

*Adamou et al  
cited with Record*

tr_ <u>Q9ANY1</u>	Pneumococcal histidine triad protein E precursor	1039
Q9ANY1_STRPN	(Hypothetical	AA
	protein SP1004) [phtE] [Streptococcus pneumoniae]	align

Score = 2016 bits (5224), Expect = 0.0  
 Identities = 1004/1039 (96%), Positives = 1004/1039 (96%)

Query: 1	MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLT	PDQVS 60
Sbjct: 1	MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLT	PDQVS 60
Query: 61	QKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMDPQVNLKDADIVN	120
Sbjct: 61	QKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMDPQVNLKDADIVN	120
Query: 121	EVKGGYIICKVTDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNAVARSQGRY	180
Sbjct: 121	EVKGGYIICKVTDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNAVARSQGRY	180
Query: 181	TTNDGYVFNPADIEEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXXNMQLPSQLS	240
Sbjct: 181	TTNDGYVFNPADIEEDTGNAYIVPHGGHYHYIP	NMQLPSQLS
Query: 241	YSSTASDNNTQSVAKGSTSKPANKSENLQSLLKELYDPSAQRYS	ESDGLVFDPAIISR 300
Sbjct: 241	YSSTASDNNTQSVAKGSTSKPANKSENLQSLLKELYDPSAQRYS	ESDGLVFDPAIISR 300
Query: 301	TPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTNAKPNEVXXXXXXX	360
Sbjct: 301	TPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTNAKPNEV	360
Query: 361	XXXXXXXXKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNSQIGQPTLPNNSLA	420
Sbjct: 361	KELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNSQIGQPTLPNNSLA	420
Query: 421	TPSPSLPINPGTSHEKHEEDGYGFDANRIIAEDESGFVMSHGDNHYFFKKDLTEEQIKA	480
Sbjct: 421	TPSPSLPINPGTSHEKHEEDGYGFDANRIIAEDESGFVMSHGDNHYFFKKDLTEEQIKA	480
Query: 481	AQKHLEEVKTSHNGLDSLSSHEQDYPSSNAEMKDLLKKIEEKIAGIMKQYGVKRESIVVN	540
Sbjct: 481	AQKHLEEVKTSHNGLDSLSSHEQDYPSSNAEMKDLLKKIEEKIAGIMKQYGVKRESIVVN	540
Query: 541	KEKNAIIIYPHGDHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV	600
Sbjct: 541	KEKNAIIIYPHGDHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV	600
Query: 601	VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVLEKVSGKVG	660
Sbjct: 601	VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVLEKVSGKVG	660
Query: 661	EGVGNIANFELDQPYLPGQTFKYTIAASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA	720
Sbjct: 661	EGVGNIANFELDQPYLPGQTFKYTIAASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA	720
Query: 721	GDTYLRVNPQFAVPKGTDALRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK	780
Sbjct: 721	GDTYLRVNPQFAVPKGTDALRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK	780

Query: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENLKLDEKVEEPKTS 840  
 Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENLKLDEKVEEPKTS 840  
  
 Query: 841 EKVEKEKLSETGNSTSNTLEEVPTVDPVQEKVAKFAESYGMKLENVLNFNMDGTIELYLP 900  
 Sbjct: 841 EKVEKEKLSETGNSTSNTLEEVPTVDPVQEKVAKFAESYGMKLENVLNFNMDGTIELYLP 900  
  
 Query: 901 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960  
 Sbjct: 901 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960  
  
 Query: 961 ENSTDNGMLNPEGNVGSDPMILDPALEEAPAVDPVQEKEKFTASYGLGLDSVIFNMDGTI 1020  
 Sbjct: 961 ENSTDNGMLNPEGNVGSDPMILDPALEEAPAVDPVQEKEKFTASYGLGLDSVIFNMDGTI 1020  
  
 Query: 1021 ELRLPSGEVIKKNLSDLIA 1039  
 Sbjct: 1021 ELRLPSGEVIKKNLSDLIA 1039

tr Q8DQ07 Pneumococcal histidine triad protein E [phtE] 1039  
 Q8DQ07\_STRR6 [Streptococcus AA  
 pneumoniae (strain ATCC BAA-255 / R6)] align

Score = 2006 bits (5196), Expect = 0.0  
 Identities = 998/1039 (96%), Positives = 1000/1039 (96%)

Query: 1 MKFSKKYIAAGSAIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTQDQVS 60  
 Sbjct: 1 MKFSKKYIAAGSAIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTQDQVS 60  
  
 Query: 61 QKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120  
 Sbjct: 61 QKEGIQAEQIVIKITDQGYVTSHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120  
  
 Query: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRY 180  
 Sbjct: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRY 180  
  
 Query: 181 TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXXNMQLSQLS 240  
 Sbjct: 181 TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIP NMQLSQLS 240  
  
 Query: 241 YSSTASDNNTQSVAKGSTSKPANKSENLQSLLKELYDSPAQRYSSES DGLVFDPAKIISR 300  
 Sbjct: 241 YSSTASDNNTQSVAKGSTSKPANKSENLQSLLKELYDSPAQRYSSES DGLVFDPAKIISR 300  
  
 Query: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTNAKPNEVXXXXXXX 360  
 Sbjct: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVSSLGSSLSSN 360  
  
 Query: 361 XXXXXXXXKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNSQIGQPTLPNNSLA 420  
 Sbjct: 361 PSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNSQIGQPTLPNNSLA 420

Query: 421 TPSPSLPINPGLSHEKHEEDGYGFDANRIIAEDESGFVMSHGDHNHYFFKKDLTEEQIKA 480  
 TPSPSLPINPGLSHEKHEEDGYGFDANRIIAEDESGF+MSHG+HNHYFFKKDLTEEQIKA  
 Sbjct: 421 TPSPSLPINPGLSHEKHEEDGYGFDANRIIAEDESGFIMSHGNHNHYFFKKDLTEEQIKA 480

Query: 481 AQKHLEEVKTSHNGLDSLSSHEQDYPNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVN 540  
 AQKHLEEVKTSHNGLDSLSSHEQDYPNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVN  
 Sbjct: 481 AQKHLEEVKTSHNGLDSLSSHEQDYPNAKEMKDLDDKKIEEKIAGIMKQYGVKRESIVVN 540

Query: 541 KEKNAAIYPHGDHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV 600  
 KEKNAAIYPHGDHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV  
 Sbjct: 541 KEKNAAIYPHGDHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV 600

Query: 601 VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVLEKVGKVG 660  
 VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVLEKVGKVG  
 Sbjct: 601 VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVLEKVGKVG 660

Query: 661 EGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720  
 EGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA  
 Sbjct: 661 EGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720

Query: 721 GDTYLRVNPQFAVPKGTDALVRVDFEHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK 780  
 GDTYLRVNPQFAVPKGTDALVRVDFEHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK  
 Sbjct: 721 GDTYLRVNPQFAVPKGTDALVRVDFEHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK 780

Query: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENKLDEKVEEPKTS 840  
 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENKLDEKVEEPKTS  
 Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840

Query: 841 EKVEKEKLSETGNSTSNTLEEVPVDVQEKVAKFAESYGMKLENVLNFMDGTIELYLP 900  
 EKVEKEKLSETGNSTSNTLEEVPVDVQEKVAKFAESYGMKLENVLNFMDGTIELYLP  
 Sbjct: 841 EKVEKEKLSETGNSTSNTLEEVPVDVQEKVAKFAESYGMKLENVLNFMDGTIELYLP 900

Query: 901 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960  
 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP  
 Sbjct: 901 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960

Query: 961 ENSTDNGMLNPEGNVGSDPMLDALEEAPAVDPVQEKEKFTASYGLGLDSVIFNMDGTI 1020  
 ENSTDNGMLNPEGNVGSDPMLDALEEAPAVDPVQEKEKFTASYGLGLDSVIFNMDGTI  
 Sbjct: 961 ENSTDNGMLNPEGNVGSDPMLDALEEAPAVDPVQEKEKFTASYGLGLDSVIFNMDGTI 1020

Query: 1021 ELRLPSGEVIKKNLSDLIA 1039  
 ELRLPSGEVIKKNLSDLIA  
 Sbjct: 1021 ELRLPSGEVIKKNLSDLIA 1039

tr Q6WNQ7	Surface protein BVH-3 [bvh-3] [Streptococcus	1039
<u>Q6WNQ7</u> STRPN	pneumoniae]	AA
		<u>align</u>

Score = 2006 bits (5196), Expect = 0.0  
 Identities = 998/1039 (96%), Positives = 1000/1039 (96%)

Query: 1 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTQDQVS 60  
 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTQDQVS  
 Sbjct: 1 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTQDQVS 60

Query: 61 QKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120  
 QKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVN  
 Sbjct: 61 QKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120

Query: 121 EVKGGYIICKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRY 180  
 EVKGGYIICKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRY  
 Sbjct: 121 EVKGGYIICKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRY 180

Query: 181 TTNDGYVFNPADIEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXXNMQPSQLS 240  
 TTNDGYVFNPADIEDTGNAYIVPHGGHYHYIP NMQPSQLS  
 Sbjct: 181 TTNDGYVFNPADIEDTGNAYIVPHGGHYHYIPKSDLSASELAAKAHLAGKNMQPSQLS 240

Query: 241 YSSTASDNNTQSVAKGSTSKPANKSENLQSLKELYDPSAQRYS ESDGLVFDPAKIISR 300  
 YSSTASDNNTQSVAKGSTSKPANKSENLQSLKELYDPSAQRYS ESDGLVFDPAKIISR  
 Sbjct: 241 YSSTASDNNTQSVAKGSTSKPANKSENLQSLKELYDPSAQRYS ESDGLVFDPAKIISR 300

Query: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPIISGTGSTVSTNAKPNEVVXXXXXXX 360  
 TPNGVAIPHGDHYHFIPYSKLSALEEKIAR VPIISGTGSTVSTNAKPNEVV  
 Sbjct: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVVSSLGSSLSSN 360

Query: 361 XXXXXXXXKELSSASDGYIFNPKDIVETATAYIVRHGDHFHYIPKSQNQIGQPTLPNNSLA 420  
 KELSSASDGYIFNPKDIVETATAYIVRHGDHFHYIPKSQNQIGQPTLPNNSLA  
 Sbjct: 361 PSSLTTSKELSSASDGYIFNPKDIVETATAYIVRHGDHFHYIPKSQNQIGQPTLPNNSLA 420

Query: 421 TPSPSLPINPGBT SHEKHEEDGYGFDANRIIAEDESFGVMSHGDHNHYFFKKDLTEEQIKA 480  
 TPSPSLPINPGBT SHEKHEEDGYGFDANRIIAEDESFG+MSHG+HNHYFFKKDLTEEQIKA  
 Sbjct: 421 TPSPSLPINPGBT SHEKHEEDGYGFDANRIIAEDESFGFIMSHGNHNHYFFKKDLTEEQIKA 480

Query: 481 AQKHLEEVKTSHNGLDSLSSHEQDYP SNAKEMKDLDDKIEEKIAGIMKQYGVKRESIVVN 540  
 AQKHLEEVKTSHNGLDSLSSHEQDYP NAKEMKDLDDKIEEKIAGIMKQYGVKRESIVVN  
 Sbjct: 481 AQKHLEEVKTSHNGLDSLSSHEQDYP GNAKEMKDLDDKIEEKIAGIMKQYGVKRESIVVN 540

Query: 541 KEKNAI IYPHGDHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV 600  
 KEKNAI IYPHGDHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV  
 Sbjct: 541 KEKNAI IYPHGDHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV 600

Query: 601 VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVKLEKVSGKVFG 660  
 VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVKLEKVSGKVFG  
 Sbjct: 601 VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVKLEKVSGKVFG 660

Query: 661 EGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720  
 EGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA  
 Sbjct: 661 EGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720

Query: 721 GDTYLRVNPQFAVPKGTDALVRVFD EFGNAYLENNYKVGEIKLPIPKLNQGTTAGNK 780  
 GDTYLRVNPQFAVPKGTDALVRVFD EFGNAYLENNYKVGEIKLPIPKLNQGTTAGNK  
 Sbjct: 721 GDTYLRVNPQFAVPKGTDALVRVFD EFGNAYLENNYKVGEIKLPIPKLNQGTTAGNK 780

Query: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENKLDEKVEEPKTS 840  
 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQEN KLDEKVEEPKTS  
 Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840

Query: 841 EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKFKAESYGMKLENVLNFMDGTIELYLP 900  
 EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKFKAESYGMKLENVLNFMDGTIELYLP  
 Sbjct: 841 EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKFKAESYGMKLENVLNFMDGTIELYLP 900

Query: 901 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960

Sbjct: 901 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960  
 Query: 961 ENSTDNGMLNPEGNVGSDPMULDPALEEAPAVDPVQEKEKFTASYGLGLDSVIFNMDGTI 1020  
 ENSTDNGMLNPEGNVGSDPMULDPALEEAPAVDPVQEKEKFTASYGLGLDSVIFNMDGTI  
 Sbjct: 961 ENSTDNGMLNPEGNVGSDPMULDPALEEAPAVDPVQEKEKFTASYGLGLDSVIFNMDGTI 1020  
 Query: 1021 ELRLPSGEVIKKNLSDLIA 1039  
 ELRLPSGEVIKKNLSDLIA  
 Sbjct: 1021 ELRLPSGEVIKKNLSDLIA 1039

tr Q6WNQ5 surface protein BVH-3 (Fragment) [bvh-3] [Streptococcus 1019  
Q6WNQ5\_STRPN pneumoniae] AA align

Score = 1974 bits (5115), Expect = 0.0  
 Identities = 981/1019 (96%), Positives = 981/1019 (96%)

Query: 21 CAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTQDQVSQKEGIQAEQIVIKITDQGYV 80  
 CAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTQDQVSQKEGIQAEQIVIKITDQGYV  
 Sbjct: 1 CAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTQDQVSQKEGIQAEQIVIKITDQGYV 60  
 Query: 81 TSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYVVYLKD 140  
 TSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYVVYLKD  
 Sbjct: 61 TSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYVVYLKD 120  
 Query: 141 AAHADNVRTKDEINRQKQEHVKDNEKVNSNAVARSQGRYTTNDGYVFNPADIIEDTGNA 200  
 AAHADNVRTKDEINRQKQEHVKDNEKVNSNAVARSQGRYTTNDGYVFNPADIIEDTGNA  
 Sbjct: 121 AAHADNVRTKDEINRQKQEHVKDNEKVNSNAVARSQGRYTTNDGYVFNPADIIEDTGNA 180  
 Query: 201 YIVPHGGHYHYIPXXXXXXXXXXXXXXXXXXXXMQPSQLSYSSSTASDNNTQSVAKGSTSK 260  
 YIVPH GRYHYIP NMQPSQLSYSSSTASDNNTQSVAKGSTSK  
 Sbjct: 181 YIVPHRGHYHYIPKSDLSASELAAKAHLAGKNMQPSQLSYSSSTASDNNTQSVAKGSTSK 240  
 Query: 261 PANKSENLQSLLKELYDSPAQRYSSESGLVFDPAKIISRTPNGVAIPHGDHYHFIPYSK 320  
 PANKSENLQSLLKELYDSPAQRYSSESGLVFDPAKIISRTPNGVAIPHGDHYHFIPYSK  
 Sbjct: 241 PANKSENLQSLLKELYDSPAQRYSSESGLVFDPAKIISRTPNGVAIPHGDHYHFIPYSK 300  
 Query: 321 LSALEEKIARMVPISGTGSTVSTNAKPNEVXXXXXXXXXXXXXXELSSASDGYIFN 380  
 LSALEEKIARMVPISGTGSTVSTNAKPNEVV KELSSASDGYIFN  
 Sbjct: 301 LSALEEKIARMVPISGTGSTVSTNAKPNEVSSLGSLSSNPSSLTTSKELSSASDGYIFN 360  
 Query: 381 PKDIVEETATAYIVRHGDHFHYIPKSQNQIGQPTLPNNSLATPSPSLPINPGTSHEKHEED 440  
 PKDIVEETATAYIVRHGDHFHYIPKSQNQIGQPTLPNNSLATPSPSLPINPGTSHEKHEED  
 Sbjct: 361 PKDIVEETATAYIVRHGDHFHYIPKSQNQIGQPTLPNNSLATPSPSLPINPGTSHEKHEED 420  
 Query: 441 GYGF DANRIIAEDESGFVM SHGDHNHYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSS 500  
 GYGF DANRIIAEDESGFVM SHGDHNHYFFKKULTEEQIKAAQKHLEEVKTSHNGLDSLSS  
 Sbjct: 421 GYGF DANRIIAEDESGFVM SHGDHNHYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSS 480  
 Query: 501 HEQDYP SNAKEMKLDKKIEEKIAGIMKQYGVKRESIVNKEKNAI IYPHGDHHADPID 560  
 HEQDYP SNAKEMKLDKKIEEKIAGIMKQYGVKRESIVNKEKNAI IYPHGDHHADPID  
 Sbjct: 481 HEQDYP SNAKEMKLDKKIEEKIAGIMKQYGVKRESIVNKEKNAI IYPHGDHHADPID 540  
 Query: 561 EH KPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNVVNLKNSTFNNQFTLANGQ 620

Sbjct: 541 EHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNVVNLLKNSTFNNQNFTLANGQ  
Sbjct: 541 EHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNVVNLLKNSTFNNQNFTLANGQ 600

Query: 621 KRVSFSPPELEKKLGINMLVKLITPDGVLEKSGKVFGEGVGNIANFELDQPYLPQQT 680  
KRVSFSPPELEKKLGINMLVKLITPDGVLEKSGKVFGEGVGNIANFELDQPYLPQQT

Sbjct: 601 KRVSFSPPELEKKLGINMLVKLITPDGVLEKSGKVFGEGVGNIANFELDQPYLPQQT 660

Query: 681 FKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHAGDTYLRVNPQFAVPKGTDAL 740  
FKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHAGDTYLRVNPQFAVPKGTDAL

Sbjct: 661 FKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHAGDTYLRVNPQFAVPKGTDAL 720

Query: 741 VRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTAGNKIPVTFMANAYLDNQSTYIVE 800  
VRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTAGNKIPVTFMANAYLDNQSTYIVE

Sbjct: 721 VRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTAGNKIPVTFMANAYLDNQSTYIVE 780

Query: 801 VPILEKENQTDKPSILPQFKRNKAQENLKLDEKVEEPKTSEKVEKEKLSETGNSTSNTL 860  
VPILEKENQTDKPSILPQFKRNKAQEN K DEKVEEPKTSEKVEKEKLSETGNSTSNTL

Sbjct: 781 VPILEKENQTDKPSILPQFKRNKAQENSKFDEKVEEPKTSEKVEKEKLSETGNSTSNTL 840

Query: 861 EEVPTVDPVQEKFVAKFAESYGMKLENVLFNMDGTIELYLPGEVIKKNMADFTGEAPQGN 920  
EEVPTVDPVQEKFVAKFAESYGMKLENVLFNMDGTIELYLPGEVIKKNMADFTGEAPQGN

Sbjct: 841 EEVPTVDPVQEKFVAKFAESYGMKLENVLFNMDGTIELYLPGEVIKKNMADFTGEAPQGN 900

Query: 921 GENKPSENGKVSTGTVENQPTENKPADSLPPEAPNEKPVKPENSTDNGMLNPEGNVGSDPM 980  
GENKPSENGKVSTGTVENQPTENKPADSLPPEAPNEKPVKPENSTDNGMLNPEGNVGSDPM

Sbjct: 901 GENKPSENGKVSTGTVENQPTENKPADSLPPEAPNEKPVKPENSTDNGMLNPEGNVGSDPM 960

Query: 981 LDPALEEAPAVDPVQEKFASGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDLIA 1039  
LDPALEEAPAVDPVQEKFASGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDLIA

Sbjct: 961 LDPALEEAPAVDPVQEKFASGLGLDSVIFNMDGTIELRLPSGEVIKKNLSDLIA 1019

&gt; 0 &lt; IntelliGenetics

&gt; 0 &lt;

FastDB - Fast pairwise comparison of sequences  
Release 5.4

Results file sp103.res made by sdavid on Wed 28 Nov 101 11:51:05 -PST.

Query sequence being compared:  
SP103 (1-447)  
Number of sequences searched:  
1  
Number of scores above cutoff:  
1Results of the initial comparison of SP103 (1-447) with:  
File : US0971235-2.pep

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N

C

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 Db 1 SYELGLYQARTVKENNVRVSYIDGRQATQKTENLTPDEVSKEGINAEQIVIKITDQGYT 60  
 Qy 68 SHGDHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKA 127  
 Db 61 SHGDHYHYNGKVPYDAIISEELLMKDPNYQLKDEDIVNEVKGGYVIKVDGKYYVYLKA 120  
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SEQ ID 56 w098/18930

Query Match 80.9%; Score 575.5; DB 4; Length 763;  
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 Qy 66 VTSHGDIHYHYNGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLK 125  
 Db 61 VTSHGDIHYHYNGKVPYDAIISEELLMKDPNYQLKDSDIVNEIKGGYVIKVNKGKYYVYLK 120  
 Qy 126 DAAHADNVRTK 136  
 Db 121 DAAHADNIRTK 131

w098/18930 SEQ ID 66



US006582706B1

(12) **United States Patent**  
Johnson et al.

(10) Patent No.: **US 6,582,706 B1**  
(45) Date of Patent: **Jun. 24, 2003**

(54) **VACCINE COMPOSITIONS COMPRISING  
*STREPTOCOCCUS PNEUMONIAE*  
POLYPEPTIDES HAVING SELECTED  
STRUCTURAL MOTIFS**

(75) Inventors: **Leslie S. Johnson, Germantown, MD  
(US); John E. Adamou, Rockville, MD  
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(73) Assignee: **MedImmune, Inc., Gaithersburg, MD  
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(\*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

(21) Appl. No.: **09/468,656**

(22) Filed: **Dec. 21, 1999**

**Related U.S. Application Data**

(60) Provisional application No. 60/113,048, filed on Dec. 21, 1998.

(51) Int. Cl.<sup>7</sup> ..... **A61K 39/09**

(52) U.S. Cl. ..... **424/244.1; 424/184.1;  
424/185.1; 424/190.1; 424/237.1; 435/69.1;  
435/320.1; 530/350; 536/23.1; 536/23.7**

(58) Field of Search ..... **424/184.1, 185.1,  
424/190.1, 237.1, 244.1; 435/69.1, 320.1;  
514/94; 530/350; 536/23.1, 23.7**

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**Primary Examiner—James Housel**

**Assistant Examiner—Ulrike Winkler**

(74) Attorney, Agent, or Firm—Elliot M. Olstein; Alan J. Grant

(57) **ABSTRACT**

A vaccine composition is disclosed that comprises polypeptides and fragments of polypeptides containing histidine triad residues or coiled-coil regions, some of which polypeptides or fragments lie between 80 and 680 residues in length. Also disclosed are processes for preventing infection caused by *S. pneumoniae* comprising administering of vaccine compositions.

11 Claims, 32 Drawing Sheets

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search*

DATE: Monday, June 20, 2005

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US006833356B1

(12) United States Patent  
Koenig et al.(10) Patent No.: US 6,833,356 B1  
(45) Date of Patent: Dec. 21, 2004(54) PNEUMOCOCCAL PROTEIN HOMOLOGS  
AND FRAGMENTS FOR VACCINES

(75) Inventors: Scott Koenig, Rockville, MD (US); Jon Heinrichs, North Potomac, MD (US); Leslie S. Johnson, Germantown, MD (US); John E. Adamou, Germantown, MD (US)

(73) Assignee: Medimmune, Inc., Gaithersburg, MD (US)

(\*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 197 days.

(21) Appl. No.: 09/645,835

(22) Filed: Aug. 25, 2000

## Related U.S. Application Data

(60) Provisional application No. 60/150,750, filed on Aug. 25, 1999.

(51) Int. Cl.<sup>7</sup> C07K 14/00; A61K 38/16

(52) U.S. Cl. 514/12; 514/2; 530/350; 424/184.1; 424/130.1; 424/243.1; 424/244.1; 536/23.1

(58) Field of Search 514/12, 2; 530/350, 530/23.1; 424/184.1, 130.1, 243.1, 244.1, 185.1; 536/23.1

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(74) Attorney, Agent, or Firm—Elliott M. Olstein; Alan J. Grant

## (57) ABSTRACT

The invention is directed to isolated polypeptides bearing sequence homology to the Sp36 protein found in pneumococcal organisms, such as *Streptococcus pneumoniae*. Polynucleotides encoding such polypeptides are also disclosed. The invention also relates to antibodies specific for the disclosed polypeptides and to uses of such antibodies in the treatment of diseases caused by staphylococci as well as group A and B streptococci. In addition, the invention relates to the use of the disclosed polypeptides in compositions and as vaccines and for prophylactic uses such as in vaccination of animals, especially humans, against a wide variety of streptococcal, staphylococcal and other diseases.

8 Claims, 9 Drawing Sheets



US-PAT-NO: 6833356

DOCUMENT-IDENTIFIER: US 6833356 B1

TITLE: Pneumococcal protein homologs and fragments for vaccines

DATE-ISSUED: December 21, 2004

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
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Heinrichs; Jon	North Potomac	MD		
Johnson; Leslie S.	Germantown	MD		
Adamou; John E.	Germantown	MD		

## ASSIGNEE-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY	TYPE CODE
Medimmune, Inc.	Gaithersburg	MD			02

APPL-NO: 09/ 645835 [PALM]

DATE FILED: August 25, 2000

## PARENT-CASE:

This application claims the priority of U.S. Provisional Application No. 60/150,750, filed Aug. 25, 1999, the disclosure of which is hereby incorporated by reference in its entirety.

INT-CL: [07] C07 K 14/00, A61 K 38/16

US-CL-ISSUED: 514/12; 514/2, 530/350, 424/184.1, 424/130.1, 424/243.1, 424/244.1, 536/23.1

US-CL-CURRENT: 514/12, 424/130.1, 424/184.1, 424/243.1, 424/244.1, 514/2, 530/350, 536/23.1

FIELD-OF-SEARCH: 514/12, 514/2, 530/350, 530/23.1, 424/184.1, 424/130.1, 424/243.1, 424/244.1, 424/185.1, 536/23.1

## PRIOR-ART-DISCLOSED:

## U.S. PATENT DOCUMENTS

PAT-NO	ISSUE-DATE	PATENTEE-NAME	US-CL
<input type="checkbox"/> <u>4694073</u>	September 1987	Bentle et al.	530/399
<input type="checkbox"/> <u>2003/0031682</u>	February 2003	Brodeur et al.	424/190.1

## FOREIGN PATENT DOCUMENTS

FOREIGN-PAT-NO	PUBN-DATE	COUNTRY	US-CL
WO 98/18930	May 1998	WO	
WO 99/42588	August 1999	WO	
WO 00/06736	February 2000	WO	

#### OTHER PUBLICATIONS

Spellerberg et al., Lmb, a protein with similarities to the Lral adhesin family, mediates attachment of streptococcus agalactiae to human laminin. Infection and Immunity Feb. 1999, vol. 67 871-878.

ART-UNIT: 1653

PRIMARY-EXAMINER: Wax; Robert A.

ASSISTANT-EXAMINER: Kam; Chih-Min

ATTY-AGENT-FIRM: Olstein; Elliott M. Grant; Alan J.

#### ABSTRACT:

The invention is directed to isolated polypeptides bearing sequence homology to the Sp36 protein found in pneumococcal organisms, such as Streptococcus pneumoniae. Polynucleotides encoding such polypeptides are also disclosed. The invention also relates to antibodies specific for the disclosed polypeptides and to uses of such antibodies in the treatment of diseases caused by staphylococci as well as group A and B streptococci. In addition, the invention relates to the use of the disclosed polypeptides in compositions and as vaccines and for prophylactic uses such as in vaccination of animals, especially humans, against a wide variety of streptococcal, staphylococcal and other diseases.

8 Claims, 7 Drawing figures

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: Entry 15 of 34

File: USPT

Dec 21, 2004

US-PAT-NO: 6833356

DOCUMENT-IDENTIFIER: US 6833356 B1

TITLE: Pneumococcal protein homologs and fragments for vaccines

DATE-ISSUED: December 21, 2004

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Koenig; Scott	Rockville	MD		
Heinrichs; Jon	North Potomac	MD		
Johnson; Leslie S.	Germantown	MD		
Adamou; John E.	Germantown	MD		

US-CL-CURRENT: 514/12; 424/130.1, 424/184.1, 424/243.1, 424/244.1, 514/2, 530/350, 536/23.1

## CLAIMS:

What is claimed is:

1. An isolated polypeptide comprising an amino acid sequence with at least 95% sequence identity to the sequence of SEQ ID NO: 4 and wherein said polypeptide binds to an antibody that is specific for Sp36 (SEQ ID NO: 7).
2. An isolated polypeptide comprising an amino acid sequence with at least 95% sequence identity to a sequence selected from the group consisting of SEQ ID NO: 2 and 4 wherein said polypeptide is identical to that found in an organism selected from the group consisting of Group A streptococci and Staphylococcus aureus and wherein said polypeptide binds to an antibody that is specific for Sp36 (SEQ ID NO: 7).
3. The isolated polypeptide of claim 2 wherein said Group A organism is Streptococcus pyogenes.
4. The isolated polypeptide of claim 2 wherein said organism is Staphylococcus aureus.
5. An isolated polypeptide comprising an amino acid sequence at least 95% identical to the sequence of SEQ ID NO: 4 and wherein said polypeptide has a sequence with at least 12.6% sequence identity to the amino acid sequence of the Sp36 protein (SEQ ID NO: 7) of Streptococcus pneumoniae and wherein said isolated polypeptide binds to an antibody that is specific for Sp36.
6. An isolated polypeptide comprising the sequence of SEQ ID NO: 2 wherein said isolated polypeptide binds to an antibody that is specific for Sp36 (SEQ ID NO: 7) of Streptococcus pneumoniae.
7. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 2.
8. An isolated polypeptide comprising the amino acid sequence of SEQ ID NO: 4.

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L9: Entry 29 of 34

File: DWPI

Feb 10, 2005

DERWENT-ACC-NO: 2003-120461

DERWENT-WEEK: 200511

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**TITLE:** New BVH-A4 proteins and genes from serotype III Group B streptococcus, useful for treating or preventing streptococcal infection in infants, pregnant women, non-pregnant adults (e.g. pneumonia), or members of dairy herd (mastitis)

INVENTOR: BOYER, M; BRODEUR, B R ; HAMEL, J ; MARTIN, D ; RIOUX, S

PATENT-ASSIGNEE: SHIRE BIOCHEM INC (SHIRN), BOYER M (BOYEI), BRODEUR B R (BRODI), HAMEL J (HAMEI), MARTIN D (MARTI), RIOUX S (RIOUI)

PRIORITY-DATA: 2001US-287712P (May 2, 2001)

[Search Selected](#)[Search All](#)[Clear](#)**PATENT-FAMILY:**

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
<input checked="" type="checkbox"/> <a href="#">JP 2005503774 W</a>	February 10, 2005		095	C12N015/09
<input checked="" type="checkbox"/> <a href="#">WO 200288178 A2</a>	November 7, 2002	E	059	C07K014/315
<input checked="" type="checkbox"/> <a href="#">EP 1390505 A2</a>	February 25, 2004	E	000	C12N015/31
<input checked="" type="checkbox"/> <a href="#">AU 2002308325 A1</a>	November 11, 2002		000	C07K014/315
<input checked="" type="checkbox"/> <a href="#">US 20040171113 A1</a>	September 2, 2004		000	C07H021/04

DESIGNATED-STATES: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR

**APPLICATION-DATA:**

PUB-NO	APPL-DATE	APPL-NO	DESCRIPTOR
JP2005503774W	May 2, 2002	2002JP-0585476	
JP2005503774W	May 2, 2002	2002WO-CA00664	
JP2005503774W		WO 200288178	Based on
WO 200288178A2	May 2, 2002	2002WO-CA00664	
EP 1390505A2	May 2, 2002	2002EP-0766595	
EP 1390505A2	May 2, 2002	2002WO-CA00664	
EP 1390505A2		WO 200288178	Based on
AU2002308325A1	May 2, 2002	2002AU-0308325	

AU2002308325A1		WO 200288178	Based on
US20040171113A1	May 2, 2002	2002WO-CA00664	
US20040171113A1	April 19, 2004	2004US-0476614	

INT-CL (IPC): A61 K 38/00; A61 K 39/00; A61 K 39/09; A61 P 31/04; C07 H 21/04; C07 K 14/315; C07 K 19/00; C12 N 1/15; C12 N 1/19; C12 N 1/21; C12 N 5/10; C12 N 15/09; C12 N 15/31; C12 N 15/63; C12 P 21/02; G01 N 33/53; G01 N 33/569; G01 N 33/68

ABSTRACTED-PUB-NO: WO 200288178A

BASIC-ABSTRACT:

NOVELTY - An isolated polypeptide (designated GBS-BVH-A4), which comprises a BVH-A4 protein polypeptide from serotype III Group B streptococcus (GBS) strain COH1, is new.

DETAILED DESCRIPTION - An isolated polypeptide (designated GBS-BVH-A4), which comprises a BVH-A4 protein polypeptide from serotype III Group B streptococcus (GBS) strain COH1 comprises:

- (a) a polypeptide comprising 1055 amino acids (I) fully defined in the specification;
- (b) a polypeptide having at least 80-95% identity to a second polypeptide having (I);
- (c) a polypeptide capable of raising antibodies having binding specificity for (I);
- (d) an epitope bearing portion of (a);
- (e) fragments or analogs of (a), (b), (c) or (d);
- (f) any of the polypeptides of (a)-(e), where the N-terminal Met residue is deleted; or
- (g) any of the polypeptide of (a)-(e), where the secretory amino acid sequence is deleted.

INDEPENDENT CLAIMS are also included for the following:

- (1) An isolated polynucleotide comprising a sequence:
  - (a) encoding the GBS-BVH-A4 polypeptide;
  - (b) having 3168 bp fully defined in the specification; or
  - (c) that is complementary of (a) or (b);
- (2) Vectors comprising the polynucleotide, where the DNA is operably linked to an expression control region;
- (3) Host cells comprising the vector;
- (4) Producing (M1) the GBS-BVH-A4 polypeptide;

(5) Chimeric polypeptides comprising two or more GBS-BVH-A4 polypeptides, or its fragments or analogs, provided that the polypeptides are linked so as to form a chimeric polypeptide;

(6) A pharmaceutical composition comprising the GBS-BVH-A4 polypeptide, and a pharmaceutical carrier, diluent or adjuvant;

(7) Diagnosing (M2) GBS bacterial infection in a host susceptible to GBS infection; and

(8) A kit comprising the GBS-BVH-A4 polypeptide for detecting or diagnosing streptococcal infection.

ACTIVITY - Antibiotic; Immunostimulant.

Test details are described but no results are given.

MECHANISM OF ACTION - Polypeptide Therapy; Vaccine.

Test details are described but no results are given.

USE - The GBS-BVH-A4 polypeptide is useful for the therapeutic or prophylactic treatment of GBS bacterial infection in a host susceptible to GBS infection. In particular, the GBS-BVH-A4 polypeptide is useful for treating or preventing GBS infection in a neonate or infant (e.g. sepsis, meningitis, pneumonia, cellulitis, osteomyelitis, septic arthritis, endocarditis or epiglottitis), in a pregnant woman (e.g. mild urinary tract infection to life-threatening sepsis and meningitis, osteomyelitis, endocarditis, amniotitis, endometritis, wound infection (post-cesarean or post-episiotomy), cellulitis or fasciitis), in a non-pregnant adult (e.g. bacteremia, skin or soft tissue infection, pneumonia, urosepsis, endocarditis, peritonitis, meningitis or emphysema), or in a member of dairy herd (e.g. mastitis). The composition or GBS-BVH-A4 polypeptide is also useful for treating or preventing streptococcal infection (all claimed). The GBS-BVH-A4 polypeptide or antibody is also useful for diagnosing GBS or streptococcal infection.

ABSTRACTED-PUB-NO: WO 200288178A

EQUIVALENT-ABSTRACTS:

CHOSEN-DRAWING: Dwg.0/2

DERWENT-CLASS: B04 D16

CPI-CODES: B04-B04C1; B04-C01G; B04-E01; B04-F0100E; B04-F01E; B04-N0300E; B04-N03E; B11-C07A; B11-C08E; B12-K04A4; B14-A01B2; B14-C03; B14-C09; B14-F01; B14-G01; B14-K01; B14-N01; B14-N07; B14-N16; B14-S06; B14-S11B; D05-C12; D05-H09; D05-H12A; D05-H12B; D05-H12E; D05-H14B; D05-H17A5; D05-H17B5; D05-H17C;

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DOCUMENT-IDENTIFIER: US 20040052781 A1

TITLE: Vaccine compositions comprising Streptococcus pneumoniae polypeptides having selected structural motifs

Abstract Paragraph:

A vaccine composition is disclosed that comprises polypeptides and fragments of polypeptides containing histidine triad residues or coiled-coil regions, some of which polypeptides or fragments lie between 80 and 680 residues in length. Also disclosed are processes for preventing infection caused by S. pneumoniae comprising administering of vaccine compositions.

Summary of Invention Paragraph:

[0002] This invention relates generally to the field of bacterial antigens and their use, for example, as immunogenic agents in humans and animals to stimulate an immune response. More specifically, it relates to the vaccination of mammalian species with a polypeptide comprising at least one conserved histidine triad residue (HxxHxH) and at least one helix-forming polypeptide obtained from Streptococcus pneumoniae as a mechanism for stimulating production of antibodies that protect the vaccine recipient against infection by a wide range of serotypes of pathogenic S. pneumoniae. Further, the invention relates to antibodies against such polypeptides useful in diagnosis and passive immune therapy with respect to diagnosing and treating such pneumococcal infections.

Summary of Invention Paragraph:

[0004] Streptococcus pneumoniae is a gram positive bacteria which is a major causative agent in invasive infections in animals and humans, such as sepsis, meningitis, otitis media and lobar pneumonia (Tuomanen et al. New Engl. J. Med. 322:1280-1284 (1995)). As part of the infective process, pneumococci readily bind to non-inflamed human epithelial cells of the upper and lower respiratory tract by binding to eukaryotic carbohydrates in a lectin-like manner (Cundell et al., Micro. Path. 17:361-374 (1994)). Conversion to invasive pneumococcal infections for bound bacteria may involve the local generation of inflammatory factors which may activate the epithelial cells to change the number and type of receptors on their surface (Cundell et al., Nature, 377:435-438 (1995)). Apparently, one such receptor, platelet activating factor (PAF) is engaged by the pneumococcal bacteria and within a very short period of time (minutes) from the appearance of PAF, pneumococci exhibit strongly enhanced adherence and invasion of tissue. Certain soluble receptor analogs have been shown to prevent the progression of pneumococcal infections (Idanpaan-Heikkila et al., J. Inf. Dis., 176:704-712 (1997)). A number of various other proteins have been suggested as being involved in the pathogenicity of S. pneumoniae. There remains a need for identifying polypeptides having epitopes in common from various strains of S. pneumoniae in order to utilize such polypeptides as vaccines to provide protection against a wide variety of S. pneumoniae.

Summary of Invention Paragraph:

[0005] In accordance with the present invention, there is provided vaccines and vaccine compositions that include polypeptides obtained from S. pneumoniae and/or variants of said polypeptides and/or active fragments of such polypeptides.

Brief Description of Drawings Paragraph:

[0013] FIG. 3 is a western blot demonstrating the ability of antisera raised against recombinant Sp36 derived from strain Norway type 4 to react with Sp36 of heterologous strains. Total cell lysates were immunoblotted with mouse antisera to Sp36. A band representing Sp36 protein was detected in all 23 S. pneumoniae strains tested, which included isolates from each of the 23 pneumococcal serotypes represented in the current polysaccharide vaccine.

Brief Description of Drawings Paragraph:

[0018] FIG. 8 shows the results of immunization of mice with PhtD recombinant protein, which leads to protection from lethal sepsis. C3H/HeJ (Panel A and B) or Balb/cByJ (Panel C) mice were immunized subcutaneously with PhtD protein (15 .mu.g in 50 .mu.l PBS emulsified in 50 .mu.l complete Freund's adjuvant (CFA)). The recombinant PhtD protein used in protection experiments consisted of 819 amino acid residues, starting with the cysteine (residue 20). A group of 10 sham-immunized mice received PBS with adjuvant. A second immunization of 15 .mu.g protein with incomplete Freund's adjuvant (IFA) was administered 3 weeks later; the sham group received PBS with IFA. Blood was drawn (retro-orbital bleed) at week 7; and sera from each group was pooled for analysis of anti-PhtD antibody by ELISA. Mice were challenged at week 8 by an intraperitoneal (i.p.) injection of approximately 550 CFU S. pneumoniae strain SJ2, serotype 6B (Panel A), 850 CFU of strain EF6796, serotype 6A (Panel B) or 450 CFU of strain EF5668, serotype 4 (Panel C). In preliminary experiments, the LD<sub>sub</sub>.50 for strain SJ2 and EF6796 were determined to be approximately 10 CFU for both strains. The LD<sub>sub</sub>.50 for strain EF5668 was determined to be <5 CFU. Survival was determined in all groups over the course of 15 days following challenge. Data are presented as the percent survival for a total of 10 mice per experimental group. Two-sample Log-rank test was used for statistical analysis comparing recombinant Pht immunized mice to sham-immunized mice.

Detail Description Paragraph:

[0033] In accordance with a further aspect of the invention, a vaccine of the type hereinabove described is administered for the purpose of preventing or treating infection caused by S. pneumoniae.

Detail Description Paragraph:

[0040] In still another aspect the present invention relates to a method of using one or more antibodies (monoclonal, polyclonal or sera) to the polypeptides of the invention as described above for the prophylaxis and/or treatment of diseases that are caused by pneumococcal bacteria. In particular, the invention relates to a method for the prophylaxis and/or treatment of infectious diseases that are caused by S. pneumoniae. In a still further preferred aspect, the invention relates to a method for the prophylaxis and/or treatment of otitis media, nasopharyngeal, bronchial infections, and the like in humans by utilizing a vaccine of the present invention.

Detail Description Paragraph:

[0054] The present invention further relates to variants of polynucleotides. The variants of the polynucleotides may be a naturally occurring allelic variant of the polynucleotides or a non-naturally occurring variant of the polynucleotides. The variants include variants in which one or more bases are substituted, deleted or inserted. Complements to such coding polynucleotides may be utilized to isolate polynucleotides encoding the same or similar polypeptides. In particular, such procedures are useful to obtain native immunogenic portions of polypeptides from different serotypes of S. pneumoniae, which is especially useful in the production of "chain" polypeptide vaccines containing multiple immunogenic segments.

Detail Description Paragraph:

[0088] The genomic DNA used as target for amplification was isolated from S. pneumoniae Norway strain (serotype 4), the same strain used for genomic sequencing. The complete sequence of the Sp36 gene (SEQ ID NO:9), and its predicted amino acid sequence (SEQ ID NO:8), are given in the Sequence Listing appended hereto. It was noted that the predicted amino acid sequence included a hydrophobic leader sequence followed by a sequence (LSVC) similar to the consensus sequence for Type II signal peptidase (LxxC, in which both x's typically represent small amino acids). Primers (listed as SEQ ID NOS:1-3) were designed that would amplify the Sp36 gene and allow its cloning into pQE10 and expression as a histidine-tagged protein lacking the signal sequence for purification by nickel-affinity chromatography. Cloning of the fragment amplified by SEQ ID Nos 1 and 3 would result in a protein

containing amino acids 2 through 800 of Sp36; cloning of the fragment amplified by SEQ ID Nos 2 and 3 would result in a protein containing amino acids 7 through 800 of Sp36 (amino acid numbers refer to SEQ ID NO:8).

Detail Description Paragraph:

[0090] In each of the three experiments shown in FIGS. 1A-1C, C3H/HeJ mice (10/group) were immunized intraperitoneally (i.p.) with Sp36 protein (15 .mu.g in 50 .mu.l PBS emulsified in 50 .mu.l complete Freund's adjuvant (CFA)). A group of 10 sham-immunized mice received PBS with adjuvant. A second immunization of 15 .mu.g protein with incomplete Freund's adjuvant (IFA) was administered 4 weeks later; the sham group received PBS with IFA. Blood was drawn (retro-orbital bleed) at weeks 3, 6, and 9; and sera from each group were pooled for analysis of anti-Sp36 antibody by ELISA. Mice were challenged at week 10 by an i.p. injection of approximately 500 CFU *S. pneumoniae* strain SJ2 (serotype 6B; provided by P. Flynn, St. Jude Children's Research Hospital, Memphis, Tenn.). In preliminary experiments, the LD<sub>sub</sub>.50 of this strain was determined to be approximately 10 CFU. Mice were monitored for 14 days for survival.

Detail Description Paragraph:

[0099] C3H/HeJ mice (10 mice/group) were passively immunized by two i.p. injections of 100 .mu.l of rabbit serum. The first injection was administered twenty-four hours before challenge with 172 cfu of *S. pneumoniae* strain SJ2, and the second injection was given four hours after challenge. FIG. 2 shows the survival of mice after infection with two different strains of pneumococci.

Detail Description Paragraph:

[0102] Conservation of Sp36 Among Strains of *S. pneumoniae*

Detail Description Paragraph:

[0105] The mouse anti-Sp36 sera detected two major bands with apparent molecular weights of 97 and 100 kDa in all 23 pneumococcal lysates tested (shown in FIG. 3). The Sp36 signals obtained from *S. pneumoniae* serotypes 1, 5, 17F and 22F were lower, indicating either that the level of Sp36 expression is reduced in these strains, or that Sp36 in these strains is antigenically different.

Detail Description Paragraph:

[0112] These experiments indicate that Sp36 is recognized by the human immune system and suggest that antibodies able to bind the Sp36 protein may be produced during natural *S. pneumoniae* infection in humans. Since the patients were infected with a variety of pneumococcal strains, these data also support the idea that Sp36 is antigenically conserved.

CLAIMS:

2. A process for preventing infection caused by *S. pneumoniae* comprising: administering the vaccine of claim 1.

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File: PGPB

Sep 4, 2003

DOCUMENT-IDENTIFIER: US 20030165528 A1  
TITLE: *Streptococcus pyogenes* antigens

**Detail Description Paragraph:**

[0110] An ORF which shares 62% with the *S. pyogenes* BVH-P1 gene was initially presented in the patent application PCT/CA99/00114 which described Group B streptococcus antigens. BVH-PL gene was also found to share homology (62% identity) with an ORF present in the genome of *S. pneumoniae* (The Institute for Genomic Research).

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DOCUMENT-IDENTIFIER: US 6582706 B1

TITLE: Vaccine compositions comprising *Streptococcus pneumoniae* polypeptides having selected structural MOTIFS

Brief Summary Text (2):

This invention relates generally to the field of bacterial antigens and their use, for example, as immunogenic agents in humans and animals to stimulate an immune response. More specifically, it relates to the vaccination of mammalian species with a polypeptide comprising at least one conserved histidine triad residue (HxxHxH-SEQ ID NO: 12) and at least one helix-forming polypeptide obtained from Streptococcus pneumoniae as a mechanism for stimulating production of antibodies that protect the vaccine recipient against infection by a wide range of serotypes of pathogenic *S. pneumoniae*. Further, the invention relates to antibodies against such polypeptides useful in diagnosis and passive immune therapy with respect to diagnosing and treating such pneumococcal infections.

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<input type="checkbox"/>	tr	<a href="#">Q9AE21</a>	_STRAG Hypothetical protein (Fragment) [Streptococcus a... 241 9e
<input type="checkbox"/>	tr	<a href="#">Q8DQ06</a>	_STRR6 Pneumococcal histidine triad protein E, truncati... 121 8e
<input type="checkbox"/>	tr	<a href="#">Q8E029</a>	_STRA5 Hypothetical protein SAG0907 [SAG0907] [Streptoc... 111 1e
<input type="checkbox"/>	tr	<a href="#">Q8E5R2</a>	_STRA3 Hypothetical protein gbs0918 [gbs0918] [Streptoc... 109 3e
<input type="checkbox"/>	tr	<a href="#">Q8P0G5</a>	_STRP8 Putative internalin A [spyM18_1373] [Streptococc... 99 4e
<input type="checkbox"/>	tr	<a href="#">Q8K714</a>	_STRP3 Putative internalin A [inlA] [Streptococcus pyog... 97 2e
<input type="checkbox"/>	tr	<a href="#">Q5XBJ5</a>	_STRP6 Internalin protein [M6_Spy1083] [Streptococcus p... 97 3e
<input type="checkbox"/>	tr	<a href="#">Q99Z76</a>	_STRPY Putative internalin A [inlA] [Streptococcus pyog... 92 9e
<input type="checkbox"/>	tr	<a href="#">Q5AWR8</a>	_EMENI Hypothetical protein [AN7262.2] [Aspergillus nid... 47 0.
<input type="checkbox"/>	tr	<a href="#">Q6HCJ0</a>	_BACHK Cell division protein [ftsK] [Bacillus thuringie... 47 0.
<input type="checkbox"/>	sp	<a href="#">P45386</a>	IGA4_HAEIN Immunoglobulin A1 protease precursor (EC 3.... 46 0.
<input type="checkbox"/>	tr	<a href="#">Q8ISF7</a>	_CAEEL 2MDa_1 protein [isof] [Caenorhabditis elegans] 46 0.

<input type="checkbox"/>	tr	<u>Q8ISF6</u>	_CAEEL 2MDa_2 protein [isof] [Caenorhabditis elegans]	46	0.
<input type="checkbox"/>	sp	<u>P16053</u>	NFM_CHICK Neurofilament triplet M protein (160 kDa neu...)	45	0.
<input type="checkbox"/>	sp	<u>Q97QP7</u>	IGA1A_STRPN Immunoglobulin A1 protease precursor (EC 3...)	44	0.
<input type="checkbox"/>	tr	<u>Q869E1</u>	_DICDI DNA ligase I (EC 6.5.1.1) (Polydeoxyribonucleoti...)	44	0.
<input type="checkbox"/>	tr	<u>Q8IB63</u>	_PLAF7 Hypothetical protein PF08_0035 [PF08_0035] [Plas...	44	0.
<input type="checkbox"/>	tr	<u>Q9VC00</u>	_DROME CG13648-PA [CG13648] [Drosophila melanogaster (F...	44	0.
<input type="checkbox"/>	tr	<u>Q5TUJ9</u>	_ANOGA ENSANGP00000029120 [ENSANGG00000022532] [Anophel...	44	0.
<input type="checkbox"/>	tr	<u>Q839C3</u>	_ENTFA N-acetylmuramoyl-L-alanine amidase, family 4 [EF...	44	0.
<input type="checkbox"/>	tr	<u>Q7PR93</u>	_ANOGA ENSANGP00000010616 [ENSANGG00000008127] [Anophel...	44	0.
<input type="checkbox"/>	tr	<u>O73793</u>	_SERCA Neurofilament medium subunit [Serinus canaria (C...	43	0.
<input type="checkbox"/>	tr	<u>Q9FN97</u>	_ARATH Transposon protein-like [Arabidopsis thaliana (M...	43	0.
<input type="checkbox"/>	tr	<u>Q54U33</u>	_DICDI Hypothetical protein [DDB0218298] [Dictyostelium...	43	0.
<input type="checkbox"/>	tr	<u>Q963T1</u>	_PLARE Glutamate-rich protein (Fragment) [GLURP] [Plasm...	43	0.
<input type="checkbox"/>	tr	<u>Q07594</u>	_ENTHI K2 protein (Fragment) [Entamoeba histolytica]	43	0.
<input type="checkbox"/>	tr	<u>Q6PK21</u>	_HUMAN OGFR protein [Homo sapiens (Human)]	43	0.
<input type="checkbox"/>	sp_vs	<u>Q9NZT2-2</u>	Splice isoform 2 of Q9NZT2 [OGFR] [Homo sapiens (...]	43	0.
<input type="checkbox"/>	sp	<u>Q9NZT2</u>	OGFR_HUMAN Opioid growth factor receptor (OGFr) (Zeta-...)	43	0.
<input type="checkbox"/>	tr	<u>Q6HBX5</u>	_BACHK Hypothetical protein [BT9727_4640] [Bacillus thu...	43	0.
<input type="checkbox"/>	tr	<u>Q7RQS8</u>	_PLAYO Retinitis pigmentosa GTPase regulator-like prote...	43	0.
<input type="checkbox"/>	tr	<u>O77320</u>	_PLAF7 Hypothetical protein MAL3P3.3 [MAL3P3.3] [Plasmo...	43	0.
<input type="checkbox"/>	tr	<u>Q5HQ74</u>	_STAEQ Pyruvate dehydrogenase complex E2 component, dih...	42	0.
<input type="checkbox"/>	tr	<u>Q9L4Z1</u>	_STAEF Pyruvate dehydrogenase complex subunit E2 [pdhc]...	42	0.
<input type="checkbox"/>	tr	<u>Q9VGW4</u>	_DROME CG14692-PA [CG14692] [Drosophila melanogaster (F...	42	0.
<input type="checkbox"/>	tr	<u>Q90307</u>	_CARAU Carassius auratus [Carassius auratus (Goldfish)]	42	0.
<input type="checkbox"/>	tr	<u>Q898B0</u>	_CLOTE Hypothetical protein CTC00555 [CTC00555] [Clostr...	42	0.
<input type="checkbox"/>	tr	<u>Q6R4Z8</u>	_CAPBU Dehydrin cor29 [Capsella bursa-pastoris (Shepher...	42	0.
<input type="checkbox"/>	tr	<u>Q50R78</u>	_ENTHI Hypothetical protein [298.t00012] [Entamoeba his...	42	0.
<input type="checkbox"/>	tr	<u>Q8MMQ1</u>	_DICDI Similar to Required for the transfer of mannosyl...	42	0.
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<input type="checkbox"/>	tr	<u>Q55K21</u>	_CRYNE Hypothetical protein [CNBK1650] [Cryptococcus ne...	42	0.
<input type="checkbox"/>	sp	<u>Q8CT13</u>	ODP2_STAEF Dihydrolipoyllysine-residue acetyltransfера...	41	0.
<input type="checkbox"/>	tr	<u>O33741</u>	_STRPN SpsA protein [Streptococcus pneumoniae]	41	0.
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<input type="checkbox"/>	sp	<u>Q28820</u>	TRDN_RABIT Triadin [TRDN] [Oryctolagus cuniculus (Rabb...)	41	0.
<input type="checkbox"/>	sp	<u>Q59947</u>	IGA1_STRRR6 Immunoglobulin A1 protease precursor (EC 3....)	41	0.
<input type="checkbox"/>	tr	<u>Q7SXW9</u>	_BRARE Wu:fc44a10 protein (Fragment) [wu:fc44a10] [Brac...	41	0.
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<input type="checkbox"/>	tr	<u>Q94674</u>	_PLAGA Thrombospondin-related anonymous protein (Fragme...)	41	0.
<input type="checkbox"/>	tr	<u>Q5WNG8</u>	_CAEBR Hypothetical protein CBG08011 [CBG08011] [Caenor...	41	0.
<input type="checkbox"/>	tr	<u>Q6BLN0</u>	_DEBHA Similar to ca CA2433 IPF12959 Candida albicans I...	41	0.
<input type="checkbox"/>	sp_vs	<u>Q28820-4</u>	Splice isoform Cardiac 3 of Q28820 [TRDN] [Orycto...]	41	0.
<input type="checkbox"/>	sp_vs	<u>Q28820-6</u>	Splice isoform Skeletal 3 of Q28820 [TRDN] [Orycto...]	41	0.
<input type="checkbox"/>	sp	<u>Q54875</u>	IGA1B_STRPN Immunoglobulin A1 protease precursor (EC 3...)	40	0.

<input type="checkbox"/>	tr	<a href="#"><u>Q568L0</u></a>	_BRARE Wu:fc44a10 [wu:fc44a10] [Brachydanio rerio (Zebr...]	40	(
<input type="checkbox"/>	tr	<a href="#"><u>Q4ZHU3</u></a>	_STAXY Biofilm-associated protein [bap] [Staphylococcus...]	40	(
<input type="checkbox"/>	tr	<a href="#"><u>Q510B7</u></a>	_ENTHI Hypothetical protein [113.t00023] [Entamoeba his...]	40	(
<input type="checkbox"/>	tr	<a href="#"><u>Q8IJ56</u></a>	_PLAF7 Glutamate-rich protein [PF10_0344] [Plasmodium f...]	40	(
<input type="checkbox"/>	tr	<a href="#"><u>Q9GUY4</u></a>	_PENJP Crustocalcin [DD4(ccn)] [Penaeus japonicus (Kuru...]	40	(
<input type="checkbox"/>	tr	<a href="#"><u>Q9GTX2</u></a>	_PLAFA Glutamate-rich protein [GLURP] [Plasmodium falci...]	40	(
<input type="checkbox"/>	tr	<a href="#"><u>Q61US9</u></a>	_CAEBR Hypothetical protein CBG05170 [CBG05170] [Caenor...]	40	(
<input type="checkbox"/>	tr	<a href="#"><u>Q6FWC0</u></a>	_CANGA Candida glabrata strain CBS138 chromosome D comp...	40	(
<input type="checkbox"/>	tr	<a href="#"><u>Q6CTI0</u></a>	_KLULA Similar to sp Q05050 Saccharomyces cerevisiae YM...	40	(
<input type="checkbox"/>	tr	<a href="#"><u>Q879S6</u></a>	_XYLFT Hemagglutinin-like secreted protein [pspA] [Xyle...	40	(
<input type="checkbox"/>	tr	<a href="#"><u>O17102</u></a>	_CAEEL Hypothetical protein F42G2.6 [F42G2.6] [Caenorha...]	40	(

CLUSTAL W (1.74) multiple sequence alignment

tr|Q9ANY3|Q9ANY3\_STRPN

DGYIFNASDIIEDTGDAYIVPHGDHYIIPKNELSASELAAAEEAYWNGK-  
 \*\*\*:\*\*\*:\*\*\*\*\*:\*\*\*\*\* . \*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*. \*:

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
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 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

-----NMQP-SQLSYSSTASD---NNTQSVAKGSTSKPANKSEN  
 -----NMQP-SQLSYSSTASD---NNTQSVAKGSTSKPANKSEN  
 -----NMQP-SQLSYSSTASD---NNTQSVAKGSTSKPANKSEN  
 -----NMQP-SQLSYSSTASD---NNTQSVAKGSTSKPANKSEN  
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 NLSNSRTYRRQNSDNTSRTNWPSVNPGBTNTNTSNNSNQASQ SND  
 NLSNSRTYRRQNSDNTSRTNWPSVNPGBTNTNTSNNSNQASQ SND  
 -----QGSRPSSSSSHNANPAQRLSEHNLTVTPTYHQN-QGEN  
 -----QGSRPSSSSSYNANPAQRLSEHNLTVTPTYHQN-QGEN  
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\* . . . : . . . . \* : . . .

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
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 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

LQSLLKELYDSPAQRYS ESDGLVFDPAKII SRTPNGVAIPHGDHYHFIP  
 LQSLLKELYDSPAQRYS ESDGLVFDPAKII SRTPNGVAIPHGDHYHFIP  
 LQSLLKELYDSPAQRYS ESDGLVFDPAKII SRTPNGVAIPHGDHYHFIP  
 LQSLLKELYDSPAQRYS ESDGLVFDPAQITSRTARGVAVPHGDHYHFIP  
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 :\*\*\*\*:\*\*\* \* :\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\* . \*\*\*:\*\*\*\*\*:\*\*\*\*\*

tr|Q8DQ07|Q8DQ07\_STRR6  
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 tr|Q9AG74|Q9AG74\_STRPN  
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 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

YSKLSALEEKIARRVPISGTGSTVSTNAKPNEVSSLGSLSSNPS---SL  
 YSKLSALEEKIARRVPISGTGSTVSTNAKPNEVSSLGSLSSNPS---SL  
 YSKLSALEEKIARMVPISGTGSTVSTNAKPNEVSSLGSLSSNPS---SL  
 YSKMSELEERIARIIPLRYRSNHWPDSRP-EQPSPQPTPEPS PG----  
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 YEQMSELEKRIARIIPLRYRSNHWPDSRP-EQPSPQSTPEPS PSpQpAP  
 YEQMSELEKRIARIIPLRYRSNHWPDSRP-EEPSPQPTPEPS PS----

\* . : \* \* : : \* : . . . : \* \* . : . . \*

tr|Q8DQ07|Q8DQ07\_STRR6  
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 tr|Q9ANY2|Q9ANY2\_STRPN  
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 TTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIIPKS NQIGQPTL  
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 NPQPAPSNPIDEK--LVKEAVRKVGDG YVFEENG VPRYI PAKD----L  
 NPQPAPSNPIDEK--LVKEAVRKVGDG YVFEENG VSRYI PAKD----L  
 -PQPAPSNPIDGK--LVKEAVRKVGDG YVFEENG VSRYI PAKD----L  
 .. . \* . : \* . . : \* . . : \* : . : \* .

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
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 SAETAAGIDSKLAKQESLSHK-----LGAKKTD--LPSSDR  
 PSETVKNLESKLSKQESVSHT-----LTAKKEN--VAPRDQ  
 SAETAAGIDSKLAKQESLSHK-----LGAKKTD--LPSSDR  
 SAETAAGIDSKLAKQESLSHK-----LGAKKTD--LPSSDR



tr|Q9ANY3|Q9ANY3\_STRPN

--KKVPLDR--MP-YNLQYTVEVK-----NGSLIIP---HYDHYHNIK  
 . . \* : ;\* . ::\*: \* : \* . : \* . :  
 FYPFHAGDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKL  
 FYPFHAGDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKL  
 FYPFHAGDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKL  
 FYPFHAGDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKL  
 FAWFDDH-----TYKAPNG-YTLEDLFATIK--YYVEHPDER----  
 FEWFDEG-----LYEAPKG-YSLEDLLATVK--YYVEHPNER----  
 FAWFDDH-----TYKAPNG-YTLEDLFATIK--YYVEHPDER----  
 FEWFDEG-----LYEAPKG-YSLEDLLATVK--YYVEHPNER----  
 FEWFDEG-----LYEAPKG-YTLEDLLATVK--YYVEHPNER----  
 FEWFDEG-----LYEAPKG-YTLEDLLATVK--YYVEHPNER----  
 \* \* . : . \* : \* : : . : \* : \* : :  
 :

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 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

PIPKLNQGTTRTAGNKPVTFMANAYLDNQSTYIVEVP---ILEKENQT  
 PIPKLNQGTTRTAGNKPVTFMANAYLDNQSTYIVEVP---ILEKENQT  
 PIPKLNQGTTRTAGNKPVTFMANAYLDNQSTYIVEVP---ILEKENQT  
 PIPKLNQGTTRTAGNKPVTFMANAYLDNQSTYIVEVP---ILEKENQT  
 --PHSDNG---WGN-----ASEHVLGKK-----DHS  
 --PHSDNG---FGN-----ASDHVQRNKNGQ-----ADTNQT  
 --PHSDNG---WGN-----ASEHVLGKK-----DHS  
 --PHSDNG---FGN-----ASDHVQRNKNGQADTNQTEKPNEEKPQT  
 --PHSDNG---FGN-----ASDHVRKNK-----VDQD  
 --PHSDNG---FGN-----ASDHVQRNKNGQ-----ADTNQT  
 \* : ;\*: \*\* \* . : : . :  
 :

tr|Q8DQ07|Q8DQ07\_STRR6  
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 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

DKPSILPQFKRNKAQENSKLDEKVEEPKTSEKVEKEKLSETGNSTSNTL  
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 DKPSILPQFKRNKAQENSFKDEKVEEPKTSEKVEKEKLSETGNSTSNTL  
 EDP-----NKNFKADEEPVVE-ETP-AEP-----  
 EKP-----NEEKPQTEKPEE-ETPREEKP-QSEKPESP-----  
 EDP-----NKNFKADEEPVVE-ETP-AEP-----  
 EKP-----EEDKEHDEVSEP--THPESDEK-ENHVGLNPS-ADN  
 SKP-----DEDKEHDEVSEP--THPESDEK-ENHAGLNPS-ADN  
 EKP-----SEEKPQTEKPEE-ETPREEKP-QSEKPESP-----  
 ..\* . : : \* :  
 :

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

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 EEVPTVDPVQEKVAKFAESYG-MKLENVLNFNMDGTIELYLPAGEVIKKNM  
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 -----E-----VPQVET---EKVEAQLKEAEVLLAKV  
 --KPTEEPEEESPEE---ESEEPQVET---EKVKEKLREAEDLLGKI  
 -----E-----VPQVET---EKVEAQLKEAEVLLAKV  
 LYKPSTDTEE-TEEEAEDTTDEAEIPQVEH---SVINAKIAEAEALLEKV  
 LYKPSTDTEE-TEEEAEDTTDEAEIPQVEN---SVINAKIADAELLK  
 --KPTEEPEE-SPEESEE-----PQVET---EKVEEKLREAEDLLGKI  
 : : \* : : : ..\* : :  
 :

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN

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 ADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVK  
 ADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVK  
 ADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVK  
 TDSS--LKANATETLAGLRNNNLTQIMDNN-SIMAAEKLALLKGS--N  
 QNPI--IKSNAKETLTGLKNLLFGTQDNN-TIMAAEKLALLKES--K  
 TDSS--LKANATETLAGLRNNNLTQIMDNN-SIMAAEKLALLKGS--N  
 TDSS--IRQNAVETLTGLKSLLLGTKDNN-TISAEVDSLLALLKES--Q  
 TDPS--IRQNAMELTGLKSLLLGTKDNN-TISAEVDSLLALLKES--Q

tr Q9ANY3 Q9ANY3_STRPN	QDPI--IKSNAKETLTGLKNMLLFGTQDNN-TIMAEAEKLLALLKES--K : ..*... . . . : * : . . . * : . . . :
tr Q8DQ07 Q8DQ07_STRR6	PENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKEKFTASYGLGL
tr Q6WNQ7 Q6WNQ7_STRPN	PENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKEKFTASYGLGL
tr Q9ANY1 Q9ANY1_STRPN	PENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKEKFTASYGLGL
tr Q6WNQ5 Q6WNQ5_STRPN	PENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKEKFTASYGLGL
tr Q8DPQ2 Q8DPQ2_STRR6	PSSVSKEKIN-----
tr Q9AG74 Q9AG74_STRPN	-----
tr Q9AHT9 Q9AHT9_STRPN	PSSVSKEKIN-----
tr Q8DQ08 Q8DQ08_STRR6	PTPIQ-----
tr Q9ANY2 Q9ANY2_STRPN	PAPIQ-----
tr Q9ANY3 Q9ANY3_STRPN	-----
tr Q8DQ07 Q8DQ07_STRR6	DSVIFNMMDGTIELRLPSGEVIKKNLSDLIA
tr Q6WNQ7 Q6WNQ7_STRPN	DSVIFNMMDGTIELRLPSGEVIKKNLSDLIA
tr Q9ANY1 Q9ANY1_STRPN	DSVIFNMMDGTIELRLPSGEVIKKNLSDLIA
tr Q6WNQ5 Q6WNQ5_STRPN	DSVIFNMMDGTIELRLPSGEVIKKNLSDLIA
tr Q8DPQ2 Q8DPQ2_STRR6	-----
tr Q9AG74 Q9AG74_STRPN	-----
tr Q9AHT9 Q9AHT9_STRPN	-----
tr Q8DQ08 Q8DQ08_STRR6	-----
tr Q9ANY2 Q9ANY2_STRPN	-----
tr Q9ANY3 Q9ANY3_STRPN	-----

## PileUp

MSF: 1080 Type: P Check: 8540 ..

Name: tr|Q8DQ07|Q8DQ07\_STRR6 oo Len: 1080 Check: 6992 Weight: 0.100  
 Name: tr|Q6WNQ7|Q6WNQ7\_STRPN oo Len: 1080 Check: 6992 Weight: 0.100  
 Name: tr|Q9ANY1|Q9ANY1\_STRPN oo Len: 1080 Check: 7347 Weight: 0.100  
 Name: tr|Q6WNQ5|Q6WNQ5\_STRPN oo Len: 1080 Check: 4063 Weight: 0.100  
 Name: tr|Q8DPQ2|Q8DPQ2\_STRR6 oo Len: 1080 Check: 1836 Weight: 0.100  
 Name: tr|Q9AG74|Q9AG74\_STRPN oo Len: 1080 Check: 8409 Weight: 0.100  
 Name: tr|Q9AHT9|Q9AHT9\_STRPN oo Len: 1080 Check: 9461 Weight: 0.100  
 Name: tr|Q8DQ08|Q8DQ08\_STRR6 oo Len: 1080 Check: 9939 Weight: 0.100  
 Name: tr|Q9ANY2|Q9ANY2\_STRPN oo Len: 1080 Check: 1016 Weight: 0.100  
 Name: tr|Q9ANY3|Q9ANY3\_STRPN oo Len: 1080 Check: 2485 Weight: 0.100

//

tr|Q8DQ07|Q8DQ07\_STRR6 ..... MKFSKKYI AAGSAVIVSL SLCAYALNQH RSQENK.DNN  
 tr|Q6WNQ7|Q6WNQ7\_STRPN ..... MKFSKKYI AAGSAVIVSL SLCAYALNQH RSQENK.DNN  
 tr|Q9ANY1|Q9ANY1\_STRPN ..... MKFSKKYI AAGSAVIVSL SLCAYALNQH RSQENK.DNN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN ..... ..... CAYALNQH RSQENK.DNN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6 MQLEISNRKR VSMKINKKYL VG.SAAALIL SVCSYELGLY QARTVK.ENN  
 tr|Q9AG74|Q9AG74\_STRPN ..... MKINKKYL VG.SAAALIL SVCSYELGLY QARTVK.ENN  
 tr|Q9AHT9|Q9AHT9\_STRPN ..... MKINKKYL VG.SAAALIL SVCSYELGLY QARTVK.ENN  
 tr|Q8DQ08|Q8DQ08\_STRR6 ..... MKINKKYL AG.SAVLAL SVCSYELGRH QAGQVKKESN  
 tr|Q9ANY2|Q9ANY2\_STRPN ..... MKINKKYL AG.SAVLAL SVCSYELGRH QAGQVKKESN  
 tr|Q9ANY3|Q9ANY3\_STRPN ..... MKINKKYL AG.SAVLAL SVCSYELGRY QAGQDKKESN

tr|Q8DQ07|Q8DQ07\_STRR6 RVSYVDGSQS SQKSENLTDP QVSQKEGIQA EQIVIKITDQ GYVTSHGDHY  
 tr|Q6WNQ7|Q6WNQ7\_STRPN RVSYVDGSQS SQKSENLTDP QVSQKEGIQA EQIVIKITDQ GYVTSHGDHY  
 tr|Q9ANY1|Q9ANY1\_STRPN RVSYVDGSQS SQKSENLTDP QVSQKEGIQA EQIVIKITDQ GYVTSHGDHY  
 tr|Q6WNQ5|Q6WNQ5\_STRPN RVSYVDGSQS SQKSENLTDP QVSQKEGIQA EQIVIKITDQ GYVTSHGDHY  
 tr|Q8DPQ2|Q8DPQ2\_STRR6 RVSYIDGKQA TQKTENLTPD EVSKREGINA EQIVIKITDQ GYVTSHGDHY  
 tr|Q9AG74|Q9AG74\_STRPN RVSYIDGKQA TQKTENLTPD EVSKREGINA EQIVIKITDQ GYVTSHGDHY  
 tr|Q9AHT9|Q9AHT9\_STRPN RVSYIDGKQA TQKTENLTPD EVSKREGINA EQIVIKITDQ GYVTSHGDHY  
 tr|Q8DQ08|Q8DQ08\_STRR6 RVSYIDGDQA GQKAENLTDP EVSKREGINA EQIVIKITDQ GYVTSHGDHY  
 tr|Q9ANY2|Q9ANY2\_STRPN RVSYIDGDQA GQKAENLTDP EVSKREGINA EQIVIKITDQ GYVTSHGDHY  
 tr|Q9ANY3|Q9ANY3\_STRPN RVAYIDGDQA GQKAENLTDP EVSKREGINA EQIVIKITDQ GYVTSHGDHY

tr|Q8DQ07|Q8DQ07\_STRR6 HYYNGKVPYD ALFSEELLMK DPNYQLKDAD IVNEVKGGYI IKVDGKYYVY  
 tr|Q6WNQ7|Q6WNQ7\_STRPN HYYNGKVPYD ALFSEELLMK DPNYQLKDAD IVNEVKGGYI IKVDGKYYVY  
 tr|Q9ANY1|Q9ANY1\_STRPN HYYNGKVPYD ALFSEELLMK DPNYQLKDAD IVNEVKGGYI IKVDGKYYVY  
 tr|Q6WNQ5|Q6WNQ5\_STRPN HYYNGKVPYD ALFSEELLMK DPNYQLKDAD IVNEVKGGYI IKVDGKYYVY  
 tr|Q8DPQ2|Q8DPQ2\_STRR6 HYYNGKVPYD AIFSEELLMK DPNYKLKDDED IVNEVKGGYV IKVDGKYYVY  
 tr|Q9AG74|Q9AG74\_STRPN HYYNGKVPYD AIISEELLMK DPNYQLKDDED IISEIKGGYV IKVDGKYYVY  
 tr|Q9AHT9|Q9AHT9\_STRPN HYYNGKVPYD AIISEELLMK DPNYKLKDDED IVNEVKGGYV IKVDGKYYVY  
 tr|Q8DQ08|Q8DQ08\_STRR6 HYYNGKVPYD AIISEELLMK DPNYQLKDSD IVNEIKGGYV IKVDGKYYVY  
 tr|Q9ANY2|Q9ANY2\_STRPN HYYNGKVPYD AIISEELLMK DPNYQLKDSD IVNEIKGGYV IKVDGKYYVY  
 tr|Q9ANY3|Q9ANY3\_STRPN HYYNGKVPYD AIISEELLMK DPNYQLKDSD IVNEIKGGYV IKVNGKYYVY

tr|Q8DQ07|Q8DQ07\_STRR6 LKDAAHADNV RTKDEINRQK QEHVKDNE... KVNSNVAV ARSQGRYTTN  
 tr|Q6WNQ7|Q6WNQ7\_STRPN LKDAAHADNV RTKDEINRQK QEHVKDNE... KVNSNVAV ARSQGRYTTN  
 tr|Q9ANY1|Q9ANY1\_STRPN LKDAAHADNV RTKDEINRQK QEHVKDNE... KVNSNVAV ARSQGRYTTN

tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

LKDAAHADNV RTKDEINRQK QEHVKDNE... .KVNSNVAV ARSQGRYTTN  
 LKDAAHADNV RTKEEINRQK QEHSQHREGG TPRNDGAVAL ARSQGRYTTD  
 LKDAAHADNV RTKEEINRQK QEHSQHREGG TPRNDGAVAL ARSQGRYTTD  
 LKDAAHADNV RTKEEINRQK QEHSQHREGG TPRNDGAVAL ARSQGRYTTD  
 LKDAAHADNI RTKEEIKRQK QERSHNHN.. .SRADNAVA ARAQGRYTTD  
 LKDAAHADNI RTKEEIKRQK QEHSHNHG. .GSNDQAVVA ARAQGRYTTD  
 LKDAAHADNI RTKEEIKRQK QERSHNHN.. .SRADNAVA ARAQGRYTTD

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

DGYVFPNPADI IEDTGNAYIV PHGGHYHYIP KSDLSASELA AAKAHLAGK.  
 DGYVFPNPADI IEDTGNAYIV PHGGHYHYIP KSDLSASELA AAKAHLAGK.  
 DGYVFPNPADI IEDTGNAYIV PHGGHYHYIP KSDLSASELA AAKAHLAGK.  
 DGYVFPNPADI IEDTGNAYIV PHRGHYHYIP KSDLSASELA AAKAHLAGK.  
 DGYIFNASDI IEDTGDAYIV PHGDHYHYIP KNELSASELA AAEAFLSGRG  
 DGYIFNASDI IEDTGDAYIV PHGDHYHYIP KNELSASELA AAKAFLSGRG  
 DGYIFNASDI IEDTGDAYIV PHGDHYHYIP KNELSASELA AAEAFLSGRG  
 DGYIFNASDI IEDTGDAYIV PHGDHYHYIP KSDLSASELA AAQAYWNGK.  
 DGYIFNASDI IEDTGDAYIV PHGDHYHYIP KNELSASELA AAEAYWNGK.  
 DGYIFNASDI IEDTGDAYIV PHGDHYHYIP KNELSASELA AAEAYWNGK.

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

..... .NMQP.SQLS YSSTASD... NNTQSVAKGS TSKPANKSEN  
 NLSNSRTYRR QNSDNTSRN WVPSVNPGBT TNTNTSNNSN TNSQASQ SND  
 NLSNSRTYRR QNSDNTSRN WVPSVNPGBT TNTNTSNNSN TNSQASQ SND  
 NLSNSRTYRR QNSDNTSRN WVPSVNPGBT TNTNTSNNSN TNSQASQ SND  
 ..... QGSRPSSSS HNANPAQPRL SENHNLTVTP TYHQN.QGEN  
 ..... QGSRPSSSS YNANPAQPRL SENHNLTVTP TYHQN.QGEN  
 ..... QGSRPSSSS YNANPAQPRL SENHNLTVTP TYHQN.QGEN

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

LQSLKELYD SPAQRYSES DGLVFDPAKI ISRTPNGVAI PHGDHYHFIP  
 IDSLLKQLYK LPLSQRHVES DGLVFDPAQI TSRTARGVAV PHGDHYHFIP  
 IDSLLKQLYK LPLSQRHVES DGLIFDPAQI TSRTANGVAV PHGDHYHFIP  
 IDSLLKQLYK LPLSQRHVES DGLVFDPAQI TSRTARGVAV PHGDHYHFIP  
 ISSLLRELYA KPLSERHVES DGLIFDPAQI TSRTANGVAV PHGDHYHFIP  
 ISSLLRELYA KPLSERHVES DGLIFDPAQI TSRTARGVAV PHGNHYHFIP  
 ISSLLRELYA KPLSERHVES DGLIFDPAQI TSRTARGVAV PHGNHYHFIP

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

YSKLSALEEK IARRVPISGT GSTVSTNAKP NEVVSSLGSL SSNPS... SL  
 YSKLSALEEK IARRVPISGT GSTVSTNAKP NEVVSSLGSL SSNPS... SL  
 YSKLSALEEK IARMVPISGT GSTVSTNAKP NEVVSSLGSL SSNPS... SL  
 YSKLSALEER IARIPIPLRYR SNHWVPDSRP .EQPSPQPTP EPSPG.....  
 YSQLSPLEEK LARIPIPLRYR SNHWVPDSRP .EQPSPQSTP EPSPSPQPAP  
 YSQMSELEER IARIPIPLRYR SNHWVPDSRP .EQPSPQPTP EPSPG.....  
 YSQLSPLEEK LARIPIPLRYR SNHWVPDSRP .EQPSPQSTP EPSPSPQPAP  
 YEQMSELEKR IARIPIPLRYR SNHWVPDSRP .EQPSPQSTP EPSPSPQPAP  
 YEQMSELEKR IARIPIPLRYR SNHWVPDSRP .EEPSPQOPTP EPSPS.....

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN

TTSKELSSAS DGYIFNPKDI VEETATAYIV RHGDHFHYIP KSNQIGQPTL  
 TTSKELSSAS DGYIFNPKDI VEETATAYIV RHGDHFHYIP KSNQIGQPTL  
 TTSKELSSAS DGYIFNPKDI VEETATAYIV RHGDHFHYIP KSNQIGQPTL

tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

TTSKELSSAS DGYIFNPKDI VEETATAYIV RHGDHFHYIP KSNQIGQPTL  
 . PQPAPNLKI DSNSSLVSQL VRKGEGYVF EEKGISRYVF AKD.....L  
 NPQPAPSNPI DEK..LVKEA VRKGDGYVF EENGVPRYIP AKD.....L  
 . PQPAPNLKI DSNSSLVSQL VRKGEGYVF EEKGISRYVF AKD.....L  
 NPQPAPSNPI DEK..LVKEA VRKGDGYVF EENGVPRYIP AKD.....L  
 NPQPAPSNPI DEK..LVKEA VRKGDGYVF EENGVSRYIP AKD.....L  
 . PQPAPSNPI DGK..LVKEA VRKGDGYVF EENGVSRYIP AKD.....L

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

PNNSLATPSP SLPINPGISH EKHEEDGYGF DANRIIAEDE SGFIMSHGNH  
 PNNSLATPSP SLPINPGISH EKHEEDGYGF DANRIIAEDE SGFIMSHGNH  
 PNNSLATPSP SLPINPGTSH EKHEEDGYGF DANRIIAEDE SGFVMSHGHDH  
 PNNSLATPSP SLPINPGTSH EKHEEDGYGF DANRIIAEDE SGFVMSHGHDH  
 PSETVKNLES KLSKQESVSH T.....LTAKKE N...VAPRDQ  
 SAETAAGIDS KLAQQESLSH K.....LGAKKT D...LPSSDR  
 PSETVKNLES KLSKQESVSH T.....LTAKKE N...VAPRDQ  
 SAETAAGIDS KLAQQESLSH K.....LGAKKT D...LPSSDR  
 SAETAAGIDS KLAQQESLSH K.....LGAKKT D...LPSSDR  
 SAETAAGIDS KLAQQESLSH K.....LGTKKT D...LPSSDR

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

NHYFFKKDLT EEQIKAAQKH LEEVKTSHNG LDSLSSHEQD YPGNAKEMKD  
 NYFFKKDLT EEQIKAAQKH LEEVKTSHNG LDSLSSHEQD YPGNAKEMKD  
 NYFFKKDLT EEQIKAAQKH LEEVKTSHNG LDSLSSHEQD YPSNAKEMKD  
 NYFFKKDLT EEQIKAAQKH LEEVKTSHNG LDSLSSHEQD YPSNAKEMKD  
 EFYDKAYNLL TEAHKALFEN .KGRNSDFQA LDKLLERLND EST.....N  
 EFYNKAYDLL ARIHQDLDN .KGRQVDFAE LDNLLERLKD VSS.....D  
 EFYDKAYNLL TEAHKALFXN .KGRNSDFQA LDKLLERLND EST.....N  
 EFYNKAYDLL ARIHQDLDN .KGRQVDFAE LDNLLERLKD VSS.....D  
 EFYNKAYDLL ARIHQDLDN .KGRQVDFAE LDNLLERLKD VPS.....D  
 EFYNKAYDLL ARIHQDLDN .KGRQVDFAE LDNLLERLKD VSS.....D

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

LDDKIEEKIA GIMKQYGVKR ESIVVNKEKN AIIYPHGDHH HADPIDEHKP  
 KEKLVDDLLA FLAPITHPER ....LGKPNS QIEYTE....DEVRIAQL  
 KVKLVDDILA FLAPIRHPER ....LGKPNA QITYTD....DEIQVAKL  
 KEKLVDDLLA FLAPITHPER ....LGKPNS QIEYTE....DEVRIAQL  
 KVKLVDDILA FLAPIRHPER ....LGKPNA QITYTD....DEIQVAKL  
 KVKLVDDILA FLAPIRHPER ....LGKPNA QITYTD....DEIQVAKL  
 KVKLVEDILA FLAPIRHPER ....LGKPNA QITYTD....DEIQVAKL

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

VGIGHSHSNY ELFKEEGVA KKEGNKVYTG EELTNVVNLL KNSTFNNQNF  
 ADK.YTSDG YIFDEHD.II SDEGD.AYVT PHMGHS.HWI GKDSLSDKEK  
 AGK.YTTEGD YIFDPRD.IT SDEGD.AYVT PHMTHS.HWI KKDSLSEAER  
 ADK.YTSDG YIFDEHD.II SDEGD.AYVT PHMGHS.HWI GKDSLSDKEK  
 AGK.YTTEGD YIFDPRD.IT SDEGD.AYVT PHMTHS.HWI KKDSLSEAER  
 AGK.YTTEGD YIFDPRD.IT SDEGD.AYVT PHMTHS.HWI KKDSLSEAER  
 AGK.YTAEDG YIFDPRD.IT SDEGD.AYVT PHMTHS.HWI KKDSLSEAER

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN

TLANGQKRVs FSFPPELEKK LGINMLVKLI TPDGKVLEKV SGKVFGEVG  
 TLANGQKRVs FSFPPELEKK LGINMLVKLI TPDGKVLEKV SGKVFGEVG  
 TLANGQKRVs FSFPPELEKK LGINMLVKLI TPDGKVLEKV SGKVFGEVG

tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

TLANGQKRVs FSFPPELEKK LGINMLVKLI TPDGKVLEKV SGKVFGEVG  
 VAAQAYTKEK GLTPPSPDAD VKAN..... PTGDSAAAI YNRVKE...  
 AAAQAYAKEK GLTPPSTDHQ DSGN..... TEAKGAEAI YNRVKA...  
 VAAQAYTKEK GLTPPSPDAD VKAN..... PTGDSAAAI YNRVKE...  
 AAAQAYAKEK GLTPPSTDHQ DSGN..... TEAKGAEAI YNRVKA...  
 AAAQAYAKEK GLTPPSTDHQ DSGN..... TEAKGAEAI YNRVKA...  
 AAAQAYAXEK GLTPPSTDHQ DSGN..... TEAKGAEAI YNRVKA...

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

NIANFELDQP YLPGQTFKYT IASKDYPEVS YDGTFTVPTS LAYKMASQTI  
 ..KRIPLVR. .LP.YMVEHT VEVK..... NGNLIIP.. HKDHYHNIK  
 ..KKVPLDR. .MP.YNLQYT VEVK..... NGSЛИIP.. HYDHYHNIK  
 ..KRIPLVR. .LP.YMVEHT VEVK..... NGNLIIP.. HKDHYHNIK  
 ..KKVPLDR. .MP.YNLQYT VEVK..... NGSЛИIP.. HYDHYHNIK  
 ..KKVPLDR. .MP.YNLQYT VEVK..... NGSЛИIP.. HYDHYHNIK  
 ..KKVPLDR. .MP.YNLQYT VEVK..... NGSЛИIP.. HYDHYHNIK

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

FYPFHAGDTY LRVNPQFAVP KGTDALVRVF DEFHGNAYLE NNYKVGEIKL  
 FAWFDDH... TYKAP NG.YTLEDLF ATIK.. YYVE HPDER....  
 FEWFDEG... LYEAP KG.YSLEDLL ATVK.. YYVE HPNER....  
 FAWFDDH... TYKAP NG.YTLEDLF ATIK.. YYVE HPDER....  
 FEWFDEG... LYEAP KG.YSLEDLL ATVK.. YYVE HPNER....  
 FEWFDEG... LYEAP KG.YTLEDLL ATVK.. YYVE HPNER....  
 FEWFDEG... LYEAP KG.YTLEDLL ATVK.. YYVE HPNER....

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

PIPKLNQGTT RTAGNKIPVT FMANAYLDNQ STYIVEVP.. .ILEKENQT  
 ..PHSDNG.. WGN..... ASEHVLGK K..... DHS  
 ..PHSDNG.. FGN..... ASDHVQRN KNGQ..... ADTNQT  
 ..PHSDNG.. WGN..... ASEHVLGK K..... DHS  
 ..PHSDNG.. FGN..... ASDHVQRN KNGQADTNQT EKPNEEKPQT  
 ..PHSDNG.. FGN..... ASDHVRKN K..... VDQD  
 ..PHSDNG.. FGN..... ASDHVQRN KNGQ..... ADTNQT

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN  
 tr|Q6WNQ5|Q6WNQ5\_STRPN  
 tr|Q8DPQ2|Q8DPQ2\_STRR6  
 tr|Q9AG74|Q9AG74\_STRPN  
 tr|Q9AHT9|Q9AHT9\_STRPN  
 tr|Q8DQ08|Q8DQ08\_STRR6  
 tr|Q9ANY2|Q9ANY2\_STRPN  
 tr|Q9ANY3|Q9ANY3\_STRPN

DKPSILPQFK RNKAQENSKL DEKVEEPKTS EKVEKEKLSE TGNSTSNSTL  
 DKPSILPQFK RNKAQENSKL DEKVEEPKTS EKVEKEKLSE TGNSTSNSTL  
 DKPSILPQFK RNKAQENLKL DEKVEEPKTS EKVEKEKLSE TGNSTSNSTL  
 DKPSILPQFK RNKAQENSKF DEKVEEPKTS EKVEKEKLSE TGNSTSNSTL  
 EDP..... NKNFKA DEEPVE..ET P.AEP.....  
 EKP..... NEEKPQ TEKPEE..ET PREEKP.QSE KPESP....  
 EDP..... NKNFKA DEEPVE..ET P.AEP.....  
 EKP..... EEDKEH DEVSEP..TH PESDEK.ENH VGLNPS.ADN  
 SKP..... DEDKEH DEVSEP..TH PESDEK.ENH AGLNPS.ADN  
 EKP..... SEEKPQ TEKPEE..ET PREEKP.QSE KPESP....

tr|Q8DQ07|Q8DQ07\_STRR6  
 tr|Q6WNQ7|Q6WNQ7\_STRPN  
 tr|Q9ANY1|Q9ANY1\_STRPN

EEVPTVDPVQ EKVAKFAESY G.MKLENVLF NMDGTIELYL PSGEVVIKKNM  
 EEVPTVDPVQ EKVAKFAESY G.MKLENVLF NMDGTIELYL PSGEVVIKKNM  
 EEVPTVDPVQ EKVAKFAESY G.MKLENVLF NMDGTIELYL PSGEVVIKKNM

tr Q6WNQ5 Q6WNQ5_STRPN	EEVPTVDPVQ EKVAKFAESY G.MKLENVLF NMDGTIELYL PSGEVIKKNM ..... . . . . . E . . . . VPQVET . . . EKVEAQL KEAEVLLAKV .. KPTEEPEEE ESPEEESPE . . . ESEEPQVET . . . EKVKEKL REAEDLLGKI ..... . . . . . E . . . . VPQVET . . . EKVEAQL KEAEVLLAKV LYKPSTDTEE . TEEEAEDETT DEAEIPQVEH . . . SVINAKI AEAEALLEKV LYKPSTDTEE . TEEEAEDETT DEAEIPQVEN . . . SVINAKI ADAEALLEKV . . KPTEEPEEE . SPEESEE . . . . PQVET . . . EKVEEKL REAEDLLGKI
tr Q8DQ07 Q8DQ07_STRR6	ADFTGEAPQG NGENKPSENG KVSTGTVENQ PTENKPADSL PEAPNEKPVK ADFTGEAPQG NGENKPSENG KVSTGTVENQ PTENKPADSL PEAPNEKPVK ADFTGEAPQG NGENKPSENG KVSTGTVENQ PTENKPADSL PEAPNEKPVK ADFTGEAPQG NGENKPSENG KVSTGTVENQ PTENKPADSL PEAPNEKPVK TDSS..LKAN ATETLAGLRN NLTLQIMDNN . SIMAEAEKL LALLKGS..N QNPI..IKSN AKETLTGLKN NLLFGTQDNN . TIMAEAEKL LALLKES..K TDSS..LKAN ATETLAGLRN NLTLQIMDNN . SIMAEAEKL LALLKGS..N TDSS..IRQN AVETLTGLKS SLLLGTDNN . TISAEVDSDL LALLKES..Q TDPS..IRQN AMETLTGLKS SLLLGTDNN . TISAEVDSDL LALLKES..Q QDPI..IKSN AKETLTGLKN NLLFGTQDNN . TIMAEAEKL LALLKES..K
tr Q8DQ07 Q8DQ07_STRR6	PENSTDNGML NPEGNVGSDP MLDPALEEAP AVDPVQEKLE KFTASYGLGL PENSTDNGML NPEGNVGSDP MLDPALEEAP AVDPVQEKLE KFTASYGLGL PENSTDNGML NPEGNVGSDP MLDPALEEAP AVDPVQEKLE KFTASYGLGL PENSTDNGML NPEGNVGSDP MLDPALEEAP AVDPVQEKLE KFTASYGLGL PSSVSKEKIN .. PSSVSKEKIN .. PTPIQ.. PAPIQ.. ..... .
tr Q8DQ07 Q8DQ07_STRR6	DSVIFNMDGT IELRLPSGEV IKKNLSDLIA DSVIFNMDGT IELRLPSGEV IKKNLSDLIA DSVIFNMDGT IELRLPSGEV IKKNLSDLIA DSVIFNMDGT IELRLPSGEV IKKNLSDLIA ..... ..... ..... ..... ..... ..... .

**Alignments**

tr Q8DQ07 Pneumococcal histidine triad protein E [phtE] [Streptococcus pneumoniae (strain ATCC BAA-255 / R6)]

align

Score = 2017 bits (5225), Expect = 0.0

Identities = 1004/1039 (96%), Positives = 1004/1039 (96%)

Query: 1	MKF SKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLT	PDQVS 60
Sbjct: 1	MKF SKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLT	PDQVS 60
Query: 61	QKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVN	120
Sbjct: 61	QKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVN	120
Query: 121	EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRY	180
Sbjct: 121	EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNVAVARSQGRY	180
Query: 181	TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXXXXXXXXMQPSQLS	240
Sbjct: 181	TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIPKSDLSASELAAKAHLAKNMQPSQLS	240
Query: 241	YSSTASDNNTQSVAKGSTSKPANKSENLSLQSLKELYDSPAQRYS	300
Sbjct: 241	YSSTASDNNTQSVAKGSTSKPANKSENLSLQSLKELYDSPAQRYS	300
Query: 301	TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVXXXXXX	360
Sbjct: 301	TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEV	360
Query: 361	XXXXXXXXKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNN	420
Sbjct: 361	PSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNN	420
Query: 421	TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDESGFIMSHGNHNHYFFKKDLTEEQIKA	480
Sbjct: 421	TPSPSLPINPGISHEKHEEDGYGFDANRIIAEDESGFIMSHGNHNHYFFKKDLTEEQIKA	480
Query: 481	AQKHLEEVKTSHNGLDSLSSHEQDYPGNNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVN	540
Sbjct: 481	AQKHLEEVKTSHNGLDSLSSHEQDYPGNNAKEMKDLDKKIEEKIAGIMKQYGVKRESIVVN	540
Query: 541	KEKNAAIYPHGDDHHADPIDEHKPGVIGHSHSNYELFKPEEGVAKKEGNKVYTGEE	600
Sbjct: 541	KEKNAAIYPHGDDHHADPIDEHKPGVIGHSHSNYELFKPEEGVAKKEGNKVYTGEE	600
Query: 601	VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVKLEVKSGKVFG	660
Sbjct: 601	VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVKLEVKSGKVFG	660
Query: 661	EGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA	720
Sbjct: 661	EGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA	720

Query: 721 GDTYLRVNPQFAVPKGTDALVRVFDEPHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK 780  
 GDTYLRVNPQFAVPKGTDALVRVFDEPHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK  
 Sbjct: 721 GDTYLRVNPQFAVPKGTDALVRVFDEPHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK 780  
 Sbjct: 721 GDTYLRVNPQFAVPKGTDALVRVFDEPHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK 780  
 Query: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840  
 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS  
 Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840  
 Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840  
 Query: 841 EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKFVAKFAESYGMKLENVLNFNMDGTIELYLP 900  
 EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKFVAKFAESYGMKLENVLNFNMDGTIELYLP  
 Sbjct: 841 EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKFVAKFAESYGMKLENVLNFNMDGTIELYLP 900  
 Sbjct: 841 EKVEKEKLSETGNSTSNSTLEEVPVDPVQEKFVAKFAESYGMKLENVLNFNMDGTIELYLP 900  
 Query: 901 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960  
 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP  
 Sbjct: 901 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960  
 Sbjct: 901 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960  
 Query: 961 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKFVAKFAESYGMKLENVLNFNMDGTI 1020  
 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKFVAKFAESYGMKLENVLNFNMDGTI  
 Sbjct: 961 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKFVAKFAESYGMKLENVLNFNMDGTI 1020  
 Sbjct: 961 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKFVAKFAESYGMKLENVLNFNMDGTI 1020  
 Query: 1021 ELRLPSGEVIKKNLSDLIA 1039  
 ELRLPSGEVIKKNLSDLIA  
 Sbjct: 1021 ELRLPSGEVIKKNLSDLIA 1039

tr Q6WNQ7 Surface protein BVH-3 [bvh-3] [Streptococcus pneumoniae] 1039 AA align

Score = 2017 bits (5225), Expect = 0.0  
 Identities = 1004/1039 (96%), Positives = 1004/1039 (96%)

Query: 1 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTPDQVS 60  
 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTPDQVS  
 Sbjct: 1 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTPDQVS 60  
 Sbjct: 1 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTPDQVS 60  
 Query: 61 QKEGIQAQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120  
 QKEGIQAQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVN  
 Sbjct: 61 QKEGIQAQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120  
 Sbjct: 61 QKEGIQAQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVN 120  
 Query: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNAVARSQGRY 180  
 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNAVARSQGRY  
 Sbjct: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNAVARSQGRY 180  
 Sbjct: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNAVARSQGRY 180  
 Query: 181 TTNDGYVFPNPADIIEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXXXXXXNMQPSQLS 240  
 TTNDGYVFPNPADIIEDTGNAYIVPHGGHYHYIP NMQPSQLS  
 Sbjct: 181 TTNDGYVFPNPADIIEDTGNAYIVPHGGHYHYIPKSDSLSELAAKAHLAGKNMQPSQLS 240  
 Sbjct: 181 TTNDGYVFPNPADIIEDTGNAYIVPHGGHYHYIPKSDSLSELAAKAHLAGKNMQPSQLS 240  
 Query: 241 YSSTASDNNTQSVAKGSTSXPANKSENLQSLLKELYDSPAQRYSEDGLVFDPAKIISR 300  
 YSSTASDNNTQSVAKGSTSXPANKSENLQSLLKELYDSPAQRYSEDGLVFDPAKIISR  
 Sbjct: 241 YSSTASDNNTQSVAKGSTSXPANKSENLQSLLKELYDSPAQRYSEDGLVFDPAKIISR 300  
 Sbjct: 241 YSSTASDNNTQSVAKGSTSXPANKSENLQSLLKELYDSPAQRYSEDGLVFDPAKIISR 300  
 Query: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVVXXXXXXX 360  
 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVV  
 Sbjct: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVVSSLGSLSSN 360  
 Sbjct: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVVSSLGSLSSN 360  
 Query: 361 XXXXXXXXELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSQNQIGQPTLPNNSLA 420

KELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA  
 Sbjct: 361 PSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420

Query: 421 TPSPLPINPGISHEKHEEDGYGFDANRIIAEDESGFIMSHGNHNHYFFKKDLTEEQIKA 480  
 TPSPLPINPGISHEKHEEDGYGFDANRIIAEDESGFIMSHGNHNHYFFKKDLTEEQIKA  
 Sbjct: 421 TPSPLPINPGISHEKHEEDGYGFDANRIIAEDESGFIMSHGNHNHYFFKKDLTEEQIKA 480

Query: 481 AQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKLDKKIEEKIAGIMKQYGVKRESIVVN 540  
 AQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKLDKKIEEKIAGIMKQYGVKRESIVVN  
 Sbjct: 481 AQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKLDKKIEEKIAGIMKQYGVKRESIVVN 540

Query: 541 KEKNAAIYPHGDHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV 600  
 KEKNAAIYPHGDHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV  
 Sbjct: 541 KEKNAAIYPHGDHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV 600

Query: 601 VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVLEKVSGKVFG 660  
 VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVLEKVSGKVFG  
 Sbjct: 601 VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVLEKVSGKVFG 660

Query: 661 EGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720  
 EGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA  
 Sbjct: 661 EGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720

Query: 721 GDTYLRVNPQFAVPKGTDALVRVDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780  
 GDTYLRVNPQFAVPKGTDALVRVDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK  
 Sbjct: 721 GDTYLRVNPQFAVPKGTDALVRVDEFHGNAYLENNYKVGEIKLPIPKLNQGTTRTAGNK 780

Query: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840  
 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS  
 Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840

Query: 841 EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKFVAKFAESYGMKLENVLNFNMDGTIELYLP 900  
 EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKFVAKFAESYGMKLENVLNFNMDGTIELYLP  
 Sbjct: 841 EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKFVAKFAESYGMKLENVLNFNMDGTIELYLP 900

Query: 901 SGEVIKKNMADFTGEAPQGNENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960  
 SGEVIKKNMADFTGEAPQGNENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP  
 Sbjct: 901 SGEVIKKNMADFTGEAPQGNENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960

Query: 961 ENSTDNGMLNPEGNVGSDPMMDPALEEAPAVDPVQEKFVAKFAESYGMKLENVLNFNMDGTI 1020  
 ENSTDNGMLNPEGNVGSDPMMDPALEEAPAVDPVQEKFVAKFAESYGMKLENVLNFNMDGTI  
 Sbjct: 961 ENSTDNGMLNPEGNVGSDPMMDPALEEAPAVDPVQEKFVAKFAESYGMKLENVLNFNMDGTI 1020

Query: 1021 ELRLPSGEVIKKNLSDLIA 1039  
 ELRLPSGEVIKKNLSDLIA  
 Sbjct: 1021 ELRLPSGEVIKKNLSDLIA 1039

tr Q9ANY1 Pneumococcal histidine triad protein E precursor  
 (Hypothetical  
 protein SP1004) [phtE] [Streptococcus pneumoniae] 1039  
 AA  
align

Score = 2006 bits (5196), Expect = 0.0  
 Identities = 998/1039 (96%), Positives = 1000/1039 (96%)

Query: 1 MKFSKKYIAAGSAIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTPDQVS 60

Sbjct: 1 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTPDQVS  
 MKFSKKYIAAGSAVIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTPDQVS 60

 Query: 61 QKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMDPQYQLKDADIVN 120  
 QKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMDPQYQLKDADIVN  
 Sbjct: 61 QKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMDPQYQLKDADIVN 120

 Query: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNAVARSQGRY 180  
 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNAVARSQGRY  
 Sbjct: 121 EVKGGYIIKVDGKYYVYLKDAAHADNVRTKDEINRQKQEHVKDNEKVNSNAVARSQGRY 180

 Query: 181 TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXXXXXXXX 240  
 TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIP NMQPSQLS  
 Sbjct: 181 TTNDGYVFNPADIIEDTGNAYIVPHGGHYHYIPKSDSLSELAAAKAHLAGKNMQPSQLS 240

 Query: 241 YSSTASDNNTQSVAKGSTSKPANKSENLSQSLKELYDSPAQRYSSESDGLVFDPAKIISR 300  
 YSSTASDNNTQSVAKGSTSKPANKSENLSQSLKELYDSPAQRYSSESDGLVFDPAKIISR  
 Sbjct: 241 YSSTASDNNTQSVAKGSTSKPANKSENLSQSLKELYDSPAQRYSSESDGLVFDPAKIISR 300

 Query: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPIISGTGSTVSTNAKPNEVVXXXXXX 360  
 TPNGVAIPHGDHYHFIPYSKLSALEEKIAR VPIISGTGSTVSTNAKPNEVV  
 Sbjct: 301 TPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPIISGTGSTVSTNAKPNEVVSSLSSN 360

 Query: 361 XXXXXXXXKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420  
 KELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA  
 Sbjct: 361 PSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA 420

 Query: 421 TPSPLPINPGISHEKHEEDGYGF DANRIIAEDESGFIMSHGNHNHYFFKDLTEEQIKA 480  
 TPSPLPINPG SHEKHEEDGYGF DANRIIAEDESGF+MSHG+HNHYFFKDLTEEQIKA  
 Sbjct: 421 TPSPLPINPGTSHEKHEEDGYGF DANRIIAEDESGFVMSHGDNHYFFKDLTEEQIKA 480

 Query: 481 AQKHLEEVKTSHNGLDSLSSHEQDYPGNNAKEMKDLDDKIEEKIAGIMKQYGVKRESIVVN 540  
 AQKHLEEVKTSHNGLDSLSSHEQDYP NAKEMKDLDDKIEEKIAGIMKQYGVKRESIVVN  
 Sbjct: 481 AQKHLEEVKTSHNGLDSLSSHEQDYPNSNAKEMKDLDDKIEEKIAGIMKQYGVKRESIVVN 540

 Query: 541 KEKNAAIYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV 600  
 KEKNAAIYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV  
 Sbjct: 541 KEKNAAIYPHGDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV 600

 Query: 601 VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVLEKVGKVFG 660  
 VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVLEKVGKVFG  
 Sbjct: 601 VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGVLEKVGKVFG 660

 Query: 661 EGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720  
 EGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA  
 Sbjct: 661 EGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA 720

 Query: 721 GDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK 780  
 GDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK  
 Sbjct: 721 GDTYLRVNPQFAVPKGTDALVRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK 780

 Query: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840  
 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQEN KLDEKVEEPKTS  
 Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENKLDEKVEEPKTS 840

 Query: 841 EKVEKEKLSETGNSTSNSTLEEVPDVQEKVAKFAESYGMKLENVLNFNMDGTIELYLP 900  
 EKVEKEKLSETGNSTSNSTLEEVPDVQEKVAKFAESYGMKLENVLNFNMDGTIELYLP  
 Sbjct: 841 EKVEKEKLSETGNSTSNSTLEEVPDVQEKVAKFAESYGMKLENVLNFNMDGTIELYLP 900

Query: 901 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960  
 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP  
 Sbjct: 901 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLPEAPNEKPVKP 960

Query: 961 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKKLEKFTASYGLGLDSVIFNMDGTI 1020  
 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKKLEKFTASYGLGLDSVIFNMDGTI  
 Sbjct: 961 ENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKKLEKFTASYGLGLDSVIFNMDGTI 1020

Query: 1021 ELRLPSGEVIKKNLSDLIA 1039  
 ELRLPSGEVIKKNLSDLIA  
 Sbjct: 1021 ELRLPSGEVIKKNLSDLIA 1039

tr Q6WNQ5 Surface protein BVH-3 (Fragment) [bvh-3] [Streptococcus pneumoniae] 1019  
 AA align

Score = 1968 bits (5099), Expect = 0.0  
 Identities = 977/1019 (95%), Positives = 979/1019 (95%)

Query: 21 CAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTQDQVSQKEGIQAEQIVIKITDQGYV 80  
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 Sbjct: 1 CAYALNQHRSQENKDNNRVSYVDGSQSSQKSENLTQDQVSQKEGIQAEQIVIKITDQGYV 60

Query: 81 TSHGDHYHYANGKVPYDALFSEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKD 140  
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Query: 141 AAHADNVRTKDEINRQKQEHVKDNEKVNSNAVARSQGRYTTNDGYVFNPADIIIEDTGNA 200  
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Query: 201 YIVPHGGHYHYIPXXXXXXXXXXXXXXXXXNMQPSQLSYSSTASDNNTQSVAKGSTSK 260  
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 Sbjct: 181 YIVPHRGHYHYIPKSDLSASELAAKAHLAGKQNMQPSQLSYSSTASDNNTQSVAKGSTSK 240

Query: 261 PANKSENLQSLLKELYDSPAQRYSSESDGLVFDPAKIISRTPNGVAIPHGDHYHFIPYSK 320  
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Query: 321 LSALEEKIARRVPISGTGSTVSTNAKPNEVVXXXXXXXXXXXXXXKELSSASDGYIFN 380  
 LSALEEKIAR VPISGTGSTVSTNAKPNEVV KELSSASDGYIFN  
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Query: 381 PKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLATPSPSLPIPNPGISHEKHEED 440  
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Query: 501 HEQDYPGNAKEMKLDKKIEEKIAGIMKQYGVKRESIVVNKEKNAAIYPHGDHHADPID 560  
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 Sbjct: 481 HEQDYP SNAKEMKLDKKIEEKIAGIMKQYGVKRESIVVNKEKNAAIYPHGDHHADPID 540

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Query: 621 KRVSPSFPPPELEKKLGINMLVKLITPDGVKLEKVGKVFGEVGNIANFELDQPYPQQT 680  
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tr Q8CWR4 Histidine Motif-Containing protein [phpA] [Streptococcus pneumoniae (strain ATCC BAA-255 / R6)] 855  
 AA align

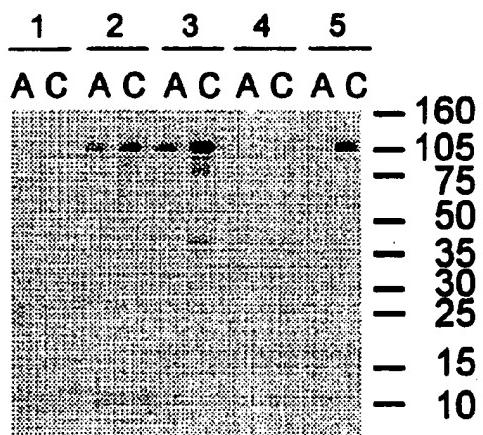
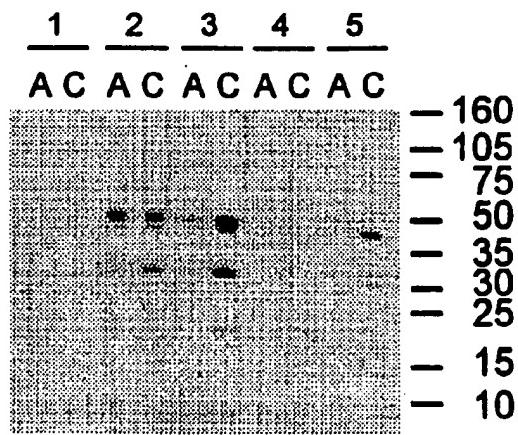
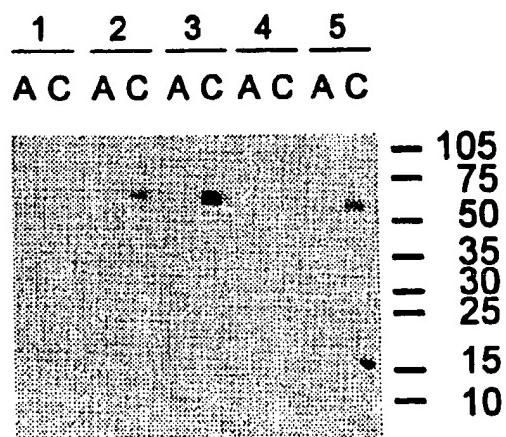
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 Identities = 219/369 (59%), Positives = 271/369 (73%), Gaps = 21/369 (5%)

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 MK +KKY+A A +V LS+CAY L H++Q K+NNRVSY+DG Q++QK+ENLTPD+VS  
 Sbjct: 12 MKINKKYLGVATLV-LSVCAYELGLHQAQTVKENNRVSYIDGKQATQKTENLTPDEVS 70

Query: 61 QKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADI 120  
 ++EGI AEQIVIKITDQGYVTSHGDHYHYYNGKVPYDA+ SEELLMKDPNYQLKD DI++  
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Query: 121 EVKGGYIIVKVDGKYYVYLKDAAHADNVRTKDEINRQKQBHVKDNE----KVNSNAVARS 176  
 E+KGGY+IKVDGKYYVYLKDAAHADNVRTK+EINRQKQEH + E + + VA+ARS  
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Query: 177 QGRYTTNDGYVFNPADIIIEDTGNAYIVPHGGHYHYIPXXXXXXXXXXXXXNMQP 236  
 QGRYTT+DGY+FN +DIIEDTG+AYIVPHG HYHYIP  
 Sbjct: 191 QGRYTTDDGYIFNASDIIIEDTGDAYIVPHGDHYHYIPKNELSASEAAKAFLSGRGNLS 250

**Figure 5****A. Full-length Sp36****B. N-terminus****C. C-terminus**

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# UniProtKB/TrEMBL

## entry Q9ANY1

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### Entry information

Entry name	<b>Q9ANY1_STRPN</b>
Primary accession number	<b>Q9ANY1</b>
Secondary accession number	Q7D4B6
Entered in TrEMBL in	Release 17, June 2001
Sequence was last modified in	Release 17, June 2001
Annotations were last modified in	Release 30, May 2005

### Name and origin of the protein

Protein name **Pneumococcal histidine triad protein E [Precursor]**

Synonym **Hypothetical protein SP1004**

Gene name **Name: phtE**

OrderedLocusNames: SP1004

From **Streptococcus pneumoniae [TaxID: 1313]**

Taxonomy **Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.**

### References

#### [1] NUCLEOTIDE SEQUENCE

DOI=10.1128/IAI.69.2.949-958.2001; PubMed=11159990 [NCBI, ExPASy, EBI, Israel, Japan]

Adamou J.E., Heinrichs J.H., Erwin A.L., Walsh W., Gayle T., Dormitzer M., Dagan R., Brewah Y.A., Barren P., Lathigra R., Langermann S., Koenig S., Johnson S.;

"Identification and characterization of a novel family of pneumococcal proteins (the Pht family) that are protective against sepsis.";

Infect. Immun. 69:949-958(2001).

#### [2] NUCLEOTIDE SEQUENCE

STRAIN=ATCC BAA-334 / TIGR4;

DOI=10.1126/science.1061217; PubMed=11463916 [NCBI, ExPASy, EBI, Israel, Japan]

Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D., Peterson S.N., Heidelberg J.F., DeBoy R.T., Haft D.H., Dodson R.J., Durkin A.S., Gwinn M.L., Kolonay J.F., Nelson W.C., Peterson J.D., Umayam L.A., White O., Salzberg S.L., Lewis M.R., Fraser C.M.;

"Complete genome sequence of a virulent isolate of *Streptococcus pneumoniae*.";

Science 293:498-506(2001).

### Comments

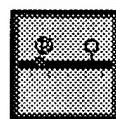
None

### Cross-references

AF318956; AAK06761.1; -;  
Genomic\_DNA.

[EMBL / GenBank / DDBJ]  
[CoCodingSequence]

EMBL	AE007403; AAK75121.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoCodingSequence]
PIR	H95115; H95115.	
TIGR	SP1004; -.	
InterPro	IPR006270; Strep_his_triad. Graphical view of domain structure.	
Pfam	PF04270; Strep_his_triad; 5. Pfam graphical view of domain structure.	
TIGRFAMs	TIGR01363; strep_his_triad; 3.	
ProDom	[Domain structure / List of seq. sharing at least 1 domain]	
HOGENOM	[Family / Alignment / Tree]	
ProtoMap	Q9ANY1.	
PRESAGE	Q9ANY1.	
ModBase	Q9ANY1.	
SWISS-2DPAGE	Get region on 2D PAGE.	
UniRef	View cluster of proteins with at least 50% / 90% identity.	

**Keywords****Complete proteome; Hypothetical protein; Signal.****Features**

Feature table viewer

Key	From	To	Length	Description
SIGNAL	1	29	29	Potential.

**Sequence information**

Length: 1039 Molecular weight: 114631 CRC64: 81A563FC806625C4 [This is a checksum on the AA sequence]

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130	140	150	160	170	180
EVKGGYIIKV	DGKYYVYLKD	AAHADNVRTK	DEINRQKQEH	VKDNEKVNSN	VAVARSQGRY
190	200	210	220	230	240
TTNDGYVFNP	ADIIIEDTGNA	YIVPHGGHYH	YIPKSDLSAS	ELAAAAKHLA	GKNMQPSQLS
250	260	270	280	290	300
YSSTASDNNT	QSVAKGSTSK	PANKSENLQS	LLKELYDSPS	AQRYSSESDGL	VFDPAKIISR
310	320	330	340	350	360
TPNGVAIPHG	DHYHFIPYSK	LSALEEKIAR	MVPISGTGST	VSTNAKPNEV	VSSLGSISSLN
370	380	390	400	410	420
PSSLTTSKEL	SSASDGYIFN	PKDIVEETAT	AYIVRHGDHF	HYIPKSNQIG	QPTLPNNSLA
430	440	450	460	470	480

TPSPSLPINP GTSHEKHEED GYGF DANRII AEDE SGFVMS HGDHNHYFFK KDLTEEQIKA  
 490 500 510 520 530 540  
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 550 560 570 580 590 600  
 KEKNAI IYPH GDHHHADPID EH KPVGIGH S HSNYEL FKPE EGVAKKEGNK VYTGEEL TNV  
 610 620 630 640 650 660  
 VNLLKNSTFN NQNFTL LANGQ KRVSF SFPPE LEKK LGINML VKLITPDGKV LEKVSG KVFG  
 670 680 690 700 710 720  
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 850 860 870 880 890 900  
 EKVEKEKLSE TGNSTS NSTL EEVPTVDPVQ EKVAKFAES Y GMKLEN VL FN MDGTIELY LP  
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 1030  
 ELRLPSGEVI KKNLSDLIA

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 BLAST	BLAST submission on ExPASy/SIB or at NCBI (USA)		Sequence analysis tools: ProtParam, ProtScale, Compute pI/Mw, PeptideMass, PeptideCutter, Dotlet (Java)
	ScanProsite, MotifScan		Submit a homology modeling request to SWISS-MODEL
	NPSA Sequence analysis tools		

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tr Q9ANY1	Pneumococcal histidine triad protein E precursor	1039
Q9ANY1_STRPN	(Hypothetical	AA
	protein SP1004) [phtE] [Streptococcus pneumoniae]	<u>align</u>

Score = 2006 bits (5196), Expect = 0.0  
 Identities = 998/1039 (96%), Positives = 1000/1039 (96%)

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	GDTYLRLVNPQFAVPKGTDALRVFDEFHGNAYLENNYKVGEIKLPI	PKLNQGTTRAGNK
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tr Q8DQ07	Pneumococcal histidine triad protein E [phtE]	1039
Q8DQ07_STRR6	[Streptococcus pneumoniae (strain ATCC BAA-255 / R6)]	AA <u>align</u>

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Query: 61	QKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALFSEELLMKDPNYQLKDADIVN	120
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	YSSTASDNNTQSVAKGSTSKPANKSENLQSLKELYDSPAQRYSedesGLVFDPAKIISR	
Sbjct: 241	YSSTASDNNTQSVAKGSTSKPANKSENLQSLKELYDSPAQRYSedesGLVFDPAKIISR	300
Query: 301	TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVXXXXXXXXX	360
	TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEV	
Sbjct: 301	TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEVSSLGSSLSSN	360
Query: 361	XXXXXXXXKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA	420
	KELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA	
Sbjct: 361	PSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHFHYIPKSNQIGQPTLPNNSLA	420
Query: 421	TPSPSLPINPGISHEKHEEDGYGF DANRIIAEDESGFIMSHGNHNHYFFKKDLTEEQIKA	480
	TPSPSLPINPGISHEKHEEDGYGF DANRIIAEDESGFIMSHGNHNHYFFKKDLTEEQIKA	
Sbjct: 421	TPSPSLPINPGISHEKHEEDGYGF DANRIIAEDESGFIMSHGNHNHYFFKKDLTEEQIKA	480
Query: 481	AQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKLDKKIEEKIAGIMKQYGVKRESIVVN	540
	AQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKLDKKIEEKIAGIMKQYGVKRESIVVN	
Sbjct: 481	AQKHLEEVKTSHNGLDSLSSHEQDYPGNAKEMKLDKKIEEKIAGIMKQYGVKRESIVVN	540
Query: 541	KEKNAI IYPHGDHHADPIDEHKPGVIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV	600
	KEKNAI IYPHGDHHADPIDEHKPGVIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV	
Sbjct: 541	KEKNAI IYPHGDHHADPIDEHKPGVIGHSHSNYELFKPEEGVAKKEGNKVTGEELTNV	600
Query: 601	VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLG INMLVKLITPDGVLEKVSGKVFG	660
	VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLG INMLVKLITPDGVLEKVSGKVFG	
Sbjct: 601	VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLG INMLVKLITPDGVLEKVSGKVFG	660
Query: 661	EGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA	720
	EGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA	
Sbjct: 661	EGVGNIANFELDQPYLPGQTFKYTIASKDYPEVSYDGTFTVPTSLAYKMASQTIFYPFHA	720
Query: 721	GDTYLRVNPQFAVPKGTDALRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK	780
	GDTYLRVNPQFAVPKGTDALRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK	
Sbjct: 721	GDTYLRVNPQFAVPKGTDALRVFDEFHGNAYLENNYKVGEIKLPIPKLNQGTTAGNK	780

Query: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840  
IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS  
Sbjct: 781 IPVTFMANAYLDNQSTYIVEVPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTS 840

Query: 841 EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLNFNMDGTIELYLP 900  
EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLNFNMDGTIELYLP  
Sbjct: 841 EKVEKEKLSETGNSTSNSTLEEVPTVDPVQEKVAKFAESYGMKLENVLNFNMDGTIELYLP 900

Query: 901 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENOPTENKPADSLPEAPNEKPVKP 960  
SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENOPTENKPADSLPEAPNEKPVKP  
Sbjct: 901 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENOPTENKPADSLPEAPNEKPVKP 960

Query: 961 ENSTDNGMLNPEGNVGSDEMLDPALEEAPAVDPVQEKFASYGLGLDSVIFNMDGTI 1020  
ENSTDNGMLNPEGNVGSDEMLDPALEEAPAVDPVQEKFASYGLGLDSVIFNMDGTI  
Sbjct: 961 ENSTDNGMLNPEGNVGSDEMLDPALEEAPAVDPVQEKFASYGLGLDSVIFNMDGTI 1020

Query: 1021 ELRLPSGEVIKKNLSDLIA 1039  
ELRLPSGEVIKKNLSDLIA  
Sbjct: 1021 ELRLPSGEVIKKNLSDLIA 1039

## CLUSTAL W (1.74) multiple sequence alignment

```

tr|Q9ANY1|Q9ANY1_STRPN MKFSKKYIAAGSAIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQK
tr|Q8DQ07|Q8DQ07_STRR6 MKFSKKYIAAGSAIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQK
tr|Q6WNQ7|Q6WNQ7_STRPN MKFSKKYIAAGSAIVSLSLCAYALNQHRSQENKDNNRVSYVDGSQSSQK
tr|Q6WNQ5|Q6WNQ5_STRPN -----CAYALNQHRSQENKDNNRVSYVDGSQSSQK
*****  

tr|Q9ANY1|Q9ANY1_STRPN SENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALF
tr|Q8DQ07|Q8DQ07_STRR6 SENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALF
tr|Q6WNQ7|Q6WNQ7_STRPN SENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALF
tr|Q6WNQ5|Q6WNQ5_STRPN SENLTPDQVSQKEGIQAEQIVIKITDQGYVTSHGDHYHYYNGKVPYDALF
*****  

tr|Q9ANY1|Q9ANY1_STRPN SEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDAAHADNVRTK
tr|Q8DQ07|Q8DQ07_STRR6 SEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDAAHADNVRTK
tr|Q6WNQ7|Q6WNQ7_STRPN SEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDAAHADNVRTK
tr|Q6WNQ5|Q6WNQ5_STRPN SEELLMKDPNYQLKDADIVNEVKGGYIIKVDGKYYVYLKDAAHADNVRTK
*****  

tr|Q9ANY1|Q9ANY1_STRPN DEINRQKQEHVKDNEKVNSNAVARSQGRYTTNDGYVFNPADIIEDTGNA
tr|Q8DQ07|Q8DQ07_STRR6 DEINRQKQEHVKDNEKVNSNAVARSQGRYTTNDGYVFNPADIIEDTGNA
tr|Q6WNQ7|Q6WNQ7_STRPN DEINRQKQEHVKDNEKVNSNAVARSQGRYTTNDGYVFNPADIIEDTGNA
tr|Q6WNQ5|Q6WNQ5_STRPN DEINRQKQEHVKDNEKVNSNAVARSQGRYTTNDGYVFNPADIIEDTGNA
*****  

tr|Q9ANY1|Q9ANY1_STRPN YIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSSTASDNNT
tr|Q8DQ07|Q8DQ07_STRR6 YIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSSTASDNNT
tr|Q6WNQ7|Q6WNQ7_STRPN YIVPHGGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSSTASDNNT
tr|Q6WNQ5|Q6WNQ5_STRPN YIVPHRGHYHYIPKSDLSASELAAAKAHLAGKNMQPSQLSYSSSTASDNNT
*****  

tr|Q9ANY1|Q9ANY1_STRPN QSVAKGSTSKPANKSENQSLLKELYDSPAQRYSES DGLVFDPAKIISR
tr|Q8DQ07|Q8DQ07_STRR6 QSVAKGSTSKPANKSENQSLLKELYDSPAQRYSES DGLVFDPAKIISR
tr|Q6WNQ7|Q6WNQ7_STRPN QSVAKGSTSKPANKSENQSLLKELYDSPAQRYSES DGLVFDPAKIISR
tr|Q6WNQ5|Q6WNQ5_STRPN QSVAKGSTSKPANKSENQSLLKELYDSPAQRYSES DGLVFDPAKIISR
*****  

tr|Q9ANY1|Q9ANY1_STRPN TPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTNAKPNEV
tr|Q8DQ07|Q8DQ07_STRR6 TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEV
tr|Q6WNQ7|Q6WNQ7_STRPN TPNGVAIPHGDHYHFIPYSKLSALEEKIARRVPISGTGSTVSTNAKPNEV
tr|Q6WNQ5|Q6WNQ5_STRPN TPNGVAIPHGDHYHFIPYSKLSALEEKIARMVPISGTGSTVSTNAKPNEV
*****  

tr|Q9ANY1|Q9ANY1_STRPN VSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHF
tr|Q8DQ07|Q8DQ07_STRR6 VSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHF
tr|Q6WNQ7|Q6WNQ7_STRPN VSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHF
tr|Q6WNQ5|Q6WNQ5_STRPN VSSLGSLSSNPSSLTTSKELSSASDGYIFNPKDIVEETATAYIVRHGDHF
*****  

tr|Q9ANY1|Q9ANY1_STRPN HYIPKSNQIGQPTLPNSLATPSPSLPINPGTSHEKHEEDGYGFDANRII
tr|Q8DQ07|Q8DQ07_STRR6 HYIPKSNQIGQPTLPNSLATPSPSLPINPGISHEKHEEDGYGFDANRII
tr|Q6WNQ7|Q6WNQ7_STRPN HYIPKSNQIGQPTLPNSLATPSPSLPINPGISHEKHEEDGYGFDANRII
tr|Q6WNQ5|Q6WNQ5_STRPN HYIPKSNQIGQPTLPNSLATPSPSLPINPGTSHEKHEEDGYGFDANRII
*****  

tr|Q9ANY1|Q9ANY1_STRPN AEDESGFVMSHGHDHNHYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSS
tr|Q8DQ07|Q8DQ07_STRR6 AEDESGFIMSHGNHNHYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSS
tr|Q6WNQ7|Q6WNQ7_STRPN AEDESGFIMSHGNHNHYFFKKDLTEEQIKAAQKHLEEVKTSHNGLDSLSS

```

tr|Q6WNQ5|Q6WNQ5\_STRPN AEDESGFVMSHGDHNHYFFKSDLTEEQIKAAQKHLEEVKTSHNGLDSLSS  
\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*  
tr|Q9ANY1|Q9ANY1\_STRPN HEQDYPNAKEMKDLDKIEEKIAGIMKQYGVKRESIVVNKEKNAI IYPH  
tr|Q8DQ07|Q8DQ07\_STRR6 HEQDYPNAKEMKDLDKIEEKIAGIMKQYGVKRESIVVNKEKNAI IYPH  
tr|Q6WNQ7|Q6WNQ7\_STRPN HEQDYPNAKEMKDLDKIEEKIAGIMKQYGVKRESIVVNKEKNAI IYPH  
tr|Q6WNQ5|Q6WNQ5\_STRPN HEQDYPNAKEMKDLDKIEEKIAGIMKQYGVKRESIVVNKEKNAI IYPH  
\*\*\*\*\*.\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*  
tr|Q9ANY1|Q9ANY1\_STRPN GDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV  
tr|Q8DQ07|Q8DQ07\_STRR6 GDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV  
tr|Q6WNQ7|Q6WNQ7\_STRPN GDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV  
tr|Q6WNQ5|Q6WNQ5\_STRPN GDHHHADPIDEHKPVGIGHSHSNYELFKPEEGVAKKEGNKVYTGEELTNV  
\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*  
tr|Q9ANY1|Q9ANY1\_STRPN VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGKV  
tr|Q8DQ07|Q8DQ07\_STRR6 VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGKV  
tr|Q6WNQ7|Q6WNQ7\_STRPN VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGKV  
tr|Q6WNQ5|Q6WNQ5\_STRPN VNLLKNSTFNNQNFTLANGQKRVSFSPPELEKKLGINMLVKLITPDGKV  
\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*  
tr|Q9ANY1|Q9ANY1\_STRPN LEKVS GTKVFGEGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFT  
tr|Q8DQ07|Q8DQ07\_STRR6 LEKVS GTKVFGEGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFT  
tr|Q6WNQ7|Q6WNQ7\_STRPN LEKVS GTKVFGEGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFT  
tr|Q6WNQ5|Q6WNQ5\_STRPN LEKVS GTKVFGEGVGNIANFELDQPYLPQTFKYTIASKDYPEVSYDGTFT  
\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*  
tr|Q9ANY1|Q9ANY1\_STRPN VPTSLAYKMASQTIFYPFHAGDTYL RVNPQFAVPKGTDALVRVFDEFGN  
tr|Q8DQ07|Q8DQ07\_STRR6 VPTSLAYKMASQTIFYPFHAGDTYL RVNPQFAVPKGTDALVRVFDEFGN  
tr|Q6WNQ7|Q6WNQ7\_STRPN VPTSLAYKMASQTIFYPFHAGDTYL RVNPQFAVPKGTDALVRVFDEFGN  
tr|Q6WNQ5|Q6WNQ5\_STRPN VPTSLAYKMASQTIFYPFHAGDTYL RVNPQFAVPKGTDALVRVFDEFGN  
\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*  
tr|Q9ANY1|Q9ANY1\_STRPN AYLENNYKVGEIKLPIPKLNQGTTAGNKPVTFMANAYLDNQSTYIVE  
tr|Q8DQ07|Q8DQ07\_STRR6 AYLENNYKVGEIKLPIPKLNQGTTAGNKPVTFMANAYLDNQSTYIVE  
tr|Q6WNQ7|Q6WNQ7\_STRPN AYLENNYKVGEIKLPIPKLNQGTTAGNKPVTFMANAYLDNQSTYIVE  
tr|Q6WNQ5|Q6WNQ5\_STRPN AYLENNYKVGEIKLPIPKLNQGTTAGNKPVTFMANAYLDNQSTYIVE  
\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*  
tr|Q9ANY1|Q9ANY1\_STRPN VPILEKENQTDKPSILPQFKRNKAQENLKLDEKVEEPKTSEKVEKEKLSE  
tr|Q8DQ07|Q8DQ07\_STRR6 VPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTSEKVEKEKLSE  
tr|Q6WNQ7|Q6WNQ7\_STRPN VPILEKENQTDKPSILPQFKRNKAQENSKLDEKVEEPKTSEKVEKEKLSE  
tr|Q6WNQ5|Q6WNQ5\_STRPN VPILEKENQTDKPSILPQFKRNKAQENSKFDEKVEEPKTSEKVEKEKLSE  
\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*  
tr|Q9ANY1|Q9ANY1\_STRPN TGNSTSNSTLEEVTVDVQEKVAKFAESYGMKLENVLFNMDGTIELYLP  
tr|Q8DQ07|Q8DQ07\_STRR6 TGNSTSNSTLEEVTVDVQEKVAKFAESYGMKLENVLFNMDGTIELYLP  
tr|Q6WNQ7|Q6WNQ7\_STRPN TGNSTSNSTLEEVTVDVQEKVAKFAESYGMKLENVLFNMDGTIELYLP  
tr|Q6WNQ5|Q6WNQ5\_STRPN TGNSTSNSTLEEVTVDVQEKVAKFAESYGMKLENVLFNMDGTIELYLP  
\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*  
tr|Q9ANY1|Q9ANY1\_STRPN SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLP  
tr|Q8DQ07|Q8DQ07\_STRR6 SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLP  
tr|Q6WNQ7|Q6WNQ7\_STRPN SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLP  
tr|Q6WNQ5|Q6WNQ5\_STRPN SGEVIKKNMADFTGEAPQGNGENKPSENGKVSTGTVENQPTENKPADSLP  
\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*  
tr|Q9ANY1|Q9ANY1\_STRPN EAPNEKPVKPENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEK  
tr|Q8DQ07|Q8DQ07\_STRR6 EAPNEKPVKPENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEK  
tr|Q6WNQ7|Q6WNQ7\_STRPN EAPNEKPVKPENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEK

tr Q6WNQ5 Q6WNQ5_STRPN	EAPNEKPVKPENSTDNGMLNPEGNVGSDPMLDPALEEAPAVDPVQEKLEK *****
tr Q9ANY1 Q9ANY1_STRPN	FTASYGLGLDSVI FNMDGTIELRLPSGEVIKKNLSDLIA
tr Q8DQ07 Q8DQ07_STRR6	FTASYGLGLDSVI FNMDGTIELRLPSGEVIKKNLSDLIA
tr Q6WNQ7 Q6WNQ7_STRPN	FTASYGLGLDSVI FNMDGTIELRLPSGEVIKKNLSDLIA
tr Q6WNQ5 Q6WNQ5_STRPN	FTASYGLGLDSVI FNMDGTIELRLPSGEVIKKNLSDLIA *****

## PileUp

MSF: 1039 Type: P Check: 304 ..

Name: tr|Q9ANY1|Q9ANY1\_STRPN oo Len: 1039 Check: 9358 Weight: 0.100  
 Name: tr|Q8DQ07|Q8DQ07\_STRR6 oo Len: 1039 Check: 8867 Weight: 0.100  
 Name: tr|Q6WNQ7|Q6WNQ7\_STRPN oo Len: 1039 Check: 8867 Weight: 0.100  
 Name: tr|Q6WNQ5|Q6WNQ5\_STRPN oo Len: 1039 Check: 3212 Weight: 0.100

//

tr|Q9ANY1|Q9ANY1\_STRPN MKFSKKYIAA GSAVIVSLSL CAYALNQHRS QENKDNNRVS YVDGSQSSQK  
 tr|Q8DQ07|Q8DQ07\_STRR6 MKFSKKYIAA GSAVIVSLSL CAYALNQHRS QENKDNNRVS YVDGSQSSQK  
 tr|Q6WNQ7|Q6WNQ7\_STRPN MKFSKKYIAA GSAVIVSLSL CAYALNQHRS QENKDNNRVS YVDGSQSSQK  
 tr|Q6WNQ5|Q6WNQ5\_STRPN ..... .... CAYALNQHRS QENKDNNRVS YVDGSQSSQK

tr|Q9ANY1|Q9ANY1\_STRPN SENLTPDQVS QKEGIQAEQI VIKITDQGYV TSHGDHYHY NGKVPYDALF  
 tr|Q8DQ07|Q8DQ07\_STRR6 SENLTPDQVS QKEGIQAEQI VIKITDQGYV TSHGDHYHY NGKVPYDALF  
 tr|Q6WNQ7|Q6WNQ7\_STRPN SENLTPDQVS QKEGIQAEQI VIKITDQGYV TSHGDHYHY NGKVPYDALF  
 tr|Q6WNQ5|Q6WNQ5\_STRPN SENLTPDQVS QKEGIQAEQI VIKITDQGYV TSHGDHYHY NGKVPYDALF

tr|Q9ANY1|Q9ANY1\_STRPN SEELLMKDPN YQLKDADIVN EVKGGYIICK DGKYYVYLKD AAHADNVRTK  
 tr|Q8DQ07|Q8DQ07\_STRR6 SEELLMKDPN YQLKDADIVN EVKGGYIICK DGKYYVYLKD AAHADNVRTK  
 tr|Q6WNQ7|Q6WNQ7\_STRPN SEELLMKDPN YQLKDADIVN EVKGGYIICK DGKYYVYLKD AAHADNVRTK  
 tr|Q6WNQ5|Q6WNQ5\_STRPN SEELLMKDPN YQLKDADIVN EVKGGYIICK DGKYYVYLKD AAHADNVRTK

tr|Q9ANY1|Q9ANY1\_STRPN DEINRQKQEH VKDNEKVNSN VAVARSQGRY TTNDGYVFNP ADIIIEDTGNA  
 tr|Q8DQ07|Q8DQ07\_STRR6 DEINRQKQEH VKDNEKVNSN VAVARSQGRY TTNDGYVFNP ADIIIEDTGNA  
 tr|Q6WNQ7|Q6WNQ7\_STRPN DEINRQKQEH VKDNEKVNSN VAVARSQGRY TTNDGYVFNP ADIIIEDTGNA  
 tr|Q6WNQ5|Q6WNQ5\_STRPN DEINRQKQEH VKDNEKVNSN VAVARSQGRY TTNDGYVFNP ADIIIEDTGNA

tr|Q9ANY1|Q9ANY1\_STRPN YIVPHGGHYH YIPKSDLSAS ELAAAKAHLA GKNMQPSQLS YSSTASDNNT  
 tr|Q8DQ07|Q8DQ07\_STRR6 YIVPHGGHYH YIPKSDLSAS ELAAAKAHLA GKNMQPSQLS YSSTASDNNT  
 tr|Q6WNQ7|Q6WNQ7\_STRPN YIVPHGGHYH YIPKSDLSAS ELAAAKAHLA GKNMQPSQLS YSSTASDNNT  
 tr|Q6WNQ5|Q6WNQ5\_STRPN YIVPHRGHYH YIPKSDLSAS ELAAAKAHLA GKNMQPSQLS YSSTASDNNT

tr|Q9ANY1|Q9ANY1\_STRPN QSVAKGSTSK PANKSENLQS LLKELYDSPS AQRYSSESDGL VFDPAKIISR  
 tr|Q8DQ07|Q8DQ07\_STRR6 QSVAKGSTSK PANKSENLQS LLKELYDSPS AQRYSSESDGL VFDPAKIISR  
 tr|Q6WNQ7|Q6WNQ7\_STRPN QSVAKGSTSK PANKSENLQS LLKELYDSPS AQRYSSESDGL VFDPAKIISR  
 tr|Q6WNQ5|Q6WNQ5\_STRPN QSVAKGSTSK PANKSENLQS LLKELYDSPS AQRYSSESDGL VFDPAKIISR

tr|Q9ANY1|Q9ANY1\_STRPN TPNGVAIPHG DHYHFIPYSK LSALEEKIAR MVPISGTGST VSTNAKPNEV  
 tr|Q8DQ07|Q8DQ07\_STRR6 TPNGVAIPHG DHYHFIPYSK LSALEEKIAR RVPISGTGST VSTNAKPNEV  
 tr|Q6WNQ7|Q6WNQ7\_STRPN TPNGVAIPHG DHYHFIPYSK LSALEEKIAR RVPISGTGST VSTNAKPNEV  
 tr|Q6WNQ5|Q6WNQ5\_STRPN TPNGVAIPHG DHYHFIPYSK LSALEEKIAR MVPISGTGST VSTNAKPNEV

tr|Q9ANY1|Q9ANY1\_STRPN VSSLGSLSSN PSSLTTSKEL SSASDGYIFN PKDIVEETAT AYIVRHGDHF  
 tr|Q8DQ07|Q8DQ07\_STRR6 VSSLGSLSSN PSSLTTSKEL SSASDGYIFN PKDIVEETAT AYIVRHGDHF  
 tr|Q6WNQ7|Q6WNQ7\_STRPN VSSLGSLSSN PSSLTTSKEL SSASDGYIFN PKDIVEETAT AYIVRHGDHF

tr|Q6WNQ5|Q6WNQ5\_STRPN

VSSLGSLSN PSSLTSKEL SSASDGYIFN PKDIVEETAT AYIVRHGDHF

tr|Q9ANY1|Q9ANY1\_STRPN  
tr|Q8DQ07|Q8DQ07\_STRR6  
tr|Q6WNQ7|Q6WNQ7\_STRPN  
tr|Q6WNQ5|Q6WNQ5\_STRPNHYIPKSNQIG QPTLPNNSLA TPSPLPINP GTSHEKHEED GYGF DANRII  
HYIPKSNQIG QPTLPNNSLA TPSPLPINP GISHEKHEED GYGF DANRII  
HYIPKSNQIG QPTLPNNSLA TPSPLPINP GISHEKHEED GYGF DANRII  
HYIPKSNQIG QPTLPNNSLA TPSPLPINP GTSHEKHEED GYGF DANRIItr|Q9ANY1|Q9ANY1\_STRPN  
tr|Q8DQ07|Q8DQ07\_STRR6  
tr|Q6WNQ7|Q6WNQ7\_STRPN  
tr|Q6WNQ5|Q6WNQ5\_STRPNAEDESGFVMS HGDHNHYFFK KDLTEEQIKA AQKHLEEVKT SHNGLDSLSS  
AEDESGFIMS HGNHNHYFFK KDLTEEQIKA AQKHLEEVKT SHNGLDSLSS  
AEDESGFIMS HGNHNHYFFK KDLTEEQIKA AQKHLEEVKT SHNGLDSLSS  
AEDESGFVMS HGDHNHYFFK KDLTEEQIKA AQKHLEEVKT SHNGLDSLSStr|Q9ANY1|Q9ANY1\_STRPN  
tr|Q8DQ07|Q8DQ07\_STRR6  
tr|Q6WNQ7|Q6WNQ7\_STRPN  
tr|Q6WNQ5|Q6WNQ5\_STRPNHEQDYPNAK EMKDLDKKIE EKIAGIMKQY GVKR ESIVVN KEKNAAIYPH  
HEQDYPNAK EMKDLDKKIE EKIAGIMKQY GVKR ESIVVN KEKNAAIYPH  
HEQDYPNAK EMKDLDKKIE EKIAGIMKQY GVKR ESIVVN KEKNAAIYPH  
HEQDYPNAK EMKDLDKKIE EKIAGIMKQY GVKR ESIVVN KEKNAAIYPHtr|Q9ANY1|Q9ANY1\_STRPN  
tr|Q8DQ07|Q8DQ07\_STRR6  
tr|Q6WNQ7|Q6WNQ7\_STRPN  
tr|Q6WNQ5|Q6WNQ5\_STRPNGDHHHADPID EH KPVGIGHS HSNYELFKPE EGVA KKEGNK VYTGEELTNV  
GDHHHADPID EH KPVGIGHS HSNYELFKPE EGVA KKEGNK VYTGEELTNV  
GDHHHADPID EH KPVGIGHS HSNYELFKPE EGVA KKEGNK VYTGEELTNV  
GDHHHADPID EH KPVGIGHS HSNYELFKPE EGVA KKEGNK VYTGEELTNVtr|Q9ANY1|Q9ANY1\_STRPN  
tr|Q8DQ07|Q8DQ07\_STRR6  
tr|Q6WNQ7|Q6WNQ7\_STRPN  
tr|Q6WNQ5|Q6WNQ5\_STRPNVNLLKNSTFN NQNFTLANGQ KRVSFSFPPE LEKKLG INML VKLITPDGKV  
VNLLKNSTFN NQNFTLANGQ KRVSFSFPPE LEKKLG INML VKLITPDGKV  
VNLLKNSTFN NQNFTLANGQ KRVSFSFPPE LEKKLG INML VKLITPDGKV  
VNLLKNSTFN NQNFTLANGQ KRVSFSFPPE LEKKLG INML VKLITPDGKVtr|Q9ANY1|Q9ANY1\_STRPN  
tr|Q8DQ07|Q8DQ07\_STRR6  
tr|Q6WNQ7|Q6WNQ7\_STRPN  
tr|Q6WNQ5|Q6WNQ5\_STRPNLEKVSGK VFG EGV GNIANFE LDQPYLPGQT FKYTIASKDY PEVSYDGTFT  
LEKVSGK VFG EGV GNIANFE LDQPYLPGQT FKYTIASKDY PEVSYDGTFT  
LEKVSGK VFG EGV GNIANFE LDQPYLPGQT FKYTIASKDY PEVSYDGTFT  
LEKVSGK VFG EGV GNIANFE LDQPYLPGQT FKYTIASKDY PEVSYDGTFTtr|Q9ANY1|Q9ANY1\_STRPN  
tr|Q8DQ07|Q8DQ07\_STRR6  
tr|Q6WNQ7|Q6WNQ7\_STRPN  
tr|Q6WNQ5|Q6WNQ5\_STRPNVPTSLAYKMA SQTIFYPFHA GDTYL RVNPQ FAVPK GTDAL VRVFDEFHGN  
VPTSLAYKMA SQTIFYPFHA GDTYL RVNPQ FAVPK GTDAL VRVFDEFHGN  
VPTSLAYKMA SQTIFYPFHA GDTYL RVNPQ FAVPK GTDAL VRVFDEFHGN  
VPTSLAYKMA SQTIFYPFHA GDTYL RVNPQ FAVPK GTDAL VRVFDEFHGNtr|Q9ANY1|Q9ANY1\_STRPN  
tr|Q8DQ07|Q8DQ07\_STRR6  
tr|Q6WNQ7|Q6WNQ7\_STRPN  
tr|Q6WNQ5|Q6WNQ5\_STRPNAYLENNYKVG EIKLPIPKLN QGTTR TAGNK IPVT FMANAY LDNQ STYIVE  
AYLENNYKVG EIKLPIPKLN QGTTR TAGNK IPVT FMANAY LDNQ STYIVE  
AYLENNYKVG EIKLPIPKLN QGTTR TAGNK IPVT FMANAY LDNQ STYIVE  
AYLENNYKVG EIKLPIPKLN QGTTR TAGNK IPVT FMANAY LDNQ STYIVEtr|Q9ANY1|Q9ANY1\_STRPN  
tr|Q8DQ07|Q8DQ07\_STRR6  
tr|Q6WNQ7|Q6WNQ7\_STRPN  
tr|Q6WNQ5|Q6WNQ5\_STRPNVPILEKENQT DKPSIL PQFK RNKAQENLKL DEKVEE PKTS EKVEKEKLSE  
VPILEKENQT DKPSIL PQFK RNKAQENS KL DEKVEE PKTS EKVEKEKLSE  
VPILEKENQT DKPSIL PQFK RNKAQENS KL DEKVEE PKTS EKVEKEKLSE  
VPILEKENQT DKPSIL PQFK RNKAQENS KF DEKVEE PKTS EKVEKEKLSEtr|Q9ANY1|Q9ANY1\_STRPN  
tr|Q8DQ07|Q8DQ07\_STRR6  
tr|Q6WNQ7|Q6WNQ7\_STRPNTGNSTS NSTL EEVPTVDPVQ EKVA KFAESY GMKLEN VLFN MDGTIELYLP  
TGNSTS NSTL EEVPTVDPVQ EKVA KFAESY GMKLEN VLFN MDGTIELYLP  
TGNSTS NSTL EEVPTVDPVQ EKVA KFAESY GMKLEN VLFN MDGTIELYLP

tr Q6WNQ5 Q6WNQ5_STRPN	TGNSTSNTL EEVPTVDPVQ EKVAKFAESY GMKLENVLFN MDGTIELYLP
tr Q9ANY1 Q9ANY1_STRPN	SGEVIKKNMA DFTGEAPQGN GENKPSENGK VSTGTVENQP TENKPADSLP
tr Q8DQ07 Q8DQ07_STRR6	SGEVIKKNMA DFTGEAPQGN GENKPSENGK VSTGTVENQP TENKPADSLP
tr Q6WNQ7 Q6WNQ7_STRPN	SGEVIKKNMA DFTGEAPQGN GENKPSENGK VSTGTVENQP TENKPADSLP
tr Q6WNQ5 Q6WNQ5_STRPN	SGEVIKKNMA DFTGEAPQGN GENKPSENGK VSTGTVENQP TENKPADSLP
tr Q9ANY1 Q9ANY1_STRPN	EAPNEKPVKP ENSTDNGMLN PEGNVGSDPM LDPALEEAPA VDPVQEKLK
tr Q8DQ07 Q8DQ07_STRR6	EAPNEKPVKP ENSTDNGMLN PEGNVGSDPM LDPALEEAPA VDPVQEKLK
tr Q6WNQ7 Q6WNQ7_STRPN	EAPNEKPVKP ENSTDNGMLN PEGNVGSDPM LDPALEEAPA VDPVQEKLK
tr Q6WNQ5 Q6WNQ5_STRPN	EAPNEKPVKP ENSTDNGMLN PEGNVGSDPM LDPALEEAPA VDPVQEKLK
tr Q9ANY1 Q9ANY1_STRPN	FTASYGLGLD SVIFNMDGTI ELRLPSGEVI KKNLSDLIA
tr Q8DQ07 Q8DQ07_STRR6	FTASYGLGLD SVIFNMDGTI ELRLPSGEVI KKNLSDLIA
tr Q6WNQ7 Q6WNQ7_STRPN	FTASYGLGLD SVIFNMDGTI ELRLPSGEVI KKNLSDLIA
tr Q6WNQ5 Q6WNQ5_STRPN	FTASYGLGLD SVIFNMDGTI ELRLPSGEVI KKNLSDLIA